

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:45:42 ; Search time 3885.92 Seconds
(without alignments)
12822.754 Million cell updates/sec

Title: US-10-767-521-2

Perfect score: 1065

Sequence: 1 atgacaacctcactagatcac.....cggaactctctatctgtctt 1065

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gsa1:*
9: gb_gsa2:*
10: gb_gsa3:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	100.0	1098	11	DQ030562 Homo sapi
2	835	78.4	867	7	CN837388 AGENCOURT
3	816.4	76.7	1002	7	CN801748 ILLUMIGEN
4	784	73.6	793	7	CN837645 AGENCOURT
5	749.8	70.3	789	2	BG205056 RST24475
6	713	66.9	884	2	BG182330 RST1196 A
7	703.8	66.1	876	3	BI906283 603063222
8	681.4	64.0	702	7	CO960092 AGENCOURT
9	669.8	62.9	675	7	CV030237 9286 Full
10	660	62.0	1761	4	AK041106 Mus muscu
11	653.6	61.4	2284	4	AK089875 Mus muscu
12	653.6	61.4	2386	4	AK089895 Mus muscu
13	651.6	61.2	745	2	BG204024 RST23417
14	540.8	50.8	1086	10	AY399291 Homo sapi
15	540.8	50.8	2583	4	CR609171 full-1eng
16	523.4	49.1	1030	11	DQ030563 Pan trogl
17	492.8	46.3	690	7	CK949072 4074244 B
18	479.8	45.1	2118	4	AK031109 Mus muscu
19	479.2	45.0	1086	10	AY399293 Mus muscu
20	479.2	45.0	2292	4	AK036597 Mus muscu
21	479.2	45.0	2432	4	AK036690 Mus muscu
22	474.6	44.6	962	1	AL552677 AL552677

23	474.4	44.5	2708	4	AK076275 Mus muscu
24	455.6	42.8	750	7	CO960088 AGENCOURT
25	455.2	42.7	832	7	CN155784 943112 MA
26	446.4	41.9	653	7	CN793072 4128034 B
27	439.2	41.2	983	5	BX337412 BX337412
28	437.2	41.1	934	2	BG460984 RST43688
29	432	40.6	1074	3	BM917063 AGENCOURT
30	418.8	39.3	731	7	CK954144 4094053 B
31	410.8	38.6	811	2	BG460103 RST42555
32	396	37.2	815	7	CO958981 AGENCOURT
33	383.8	36.0	816	5	BX340358 BX340358
34	376.6	35.4	1065	10	AY399290 Mus muscu
35	363.6	34.1	687	6	CF768885 CES001048
36	363.4	34.1	1059	10	AY399288 Homo sapi
37	362.6	34.0	1059	10	AY399289 Pan trogl
38	350.4	32.9	1083	10	AY398810 Mus muscu
39	350.4	32.9	1083	10	AY398810 Mus muscu
40	349.2	32.8	727	5	BY751590 BY751590
41	348.8	32.8	1083	10	AY398808 Homo sapi
42	344	32.3	1083	10	AY398809 Pan trogl
43	330.8	31.1	657	7	CO683220 DG11-166f
44	325	30.5	581	3	BP306915 BP306915
45	324	30.4	733	8	DN996892 TC119287

ALIGNMENTS

RESULT 1	DQ030562	1098 bp	DNA	linear	GSS 02-JUN-2005
LOCUS	DQ030562				
DEFINITION	Homo sapiens CCR3 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	DQ030562				
VERSION	DQ030562.1	GI:66881766			
KEYWORDS	GSS.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Hubisz, M.J., Bustamante, C., Clark, A.G., Gnanowski, S., Sackton, T.B., Nielsen, R., Fledel-Alon, A., Tanenbaum, D.M., Civejello, D., White, T.J., Snihey, J.J., Adams, M.D. and Cargill, M. A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (ex) PLoS Biol. 3 (6), E170 (2005)				
AUTHORS	Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejello, D., White, T.J., Snihey, J.J., Adams, M.D. and Cargill, M.				
TITLE	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
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gene	/orgnism="Homo sapiens"				
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	/chromosome="3"				
	<1..>1098				
	/gene="CCR3"				
	/locus_tag="HC336"				
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	Best Local Similarity	100.0%;	Pred. No. 7e-297;		
	Matches 1065;	Conservative	0,	Mismatches	0;
				Indels	0;
				Gaps	0;

1 ATGACAACCTCACTAGATACAGTTGAGACCTTGGTACCAATCTTACTATGATGACGTG 60
DB 31 ATGACAACCTCACTAGATACAGTTGAGACCTTGGTACCAATCTTACTATGATGACGTG 90
QY 61 GGGCTGCTCTGTGAAAAAGCTGATACCAAGACCTGATGCGCCAGTTTGGCCCCGCTG 120
DB 91 GGGCTGCTCTGTGAAAAAGCTGATACCAAGACCTGATGCGCCAGTTTGGCCCCGCTG 150
QY 121 TACTCCCTGTGTGCTGTGGGCGCTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 151 TACTCCCTGTGTGCTGTGGGCGCTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGT 210
QY 181 AATAACAGAGGCTCCGAATTATGACCAATCTTACTGCTCAACCTGGCCATTTGCGAC 240
DB 211 AATAACAGAGGCTCCGAATTATGACCAATCTTACTGCTCAACCTGGCCATTTGCGAC 270
QY 241 CTGCTCTTCTGTGCAACCTTCCATTTCTGATTCCTATGTCCAGGGGCGATTACTGGGTT 300
DB 271 CTGCTCTTCTGTGCAACCTTCCATTTCTGATTCCTATGTCCAGGGGCGATTACTGGGTT 330
QY 301 TTGGGCGATGGAGTGTAAAGCTCTGAGGGTTTATGACAGGGCTTGTACAGCGAG 360
DB 331 TTGGGCGATGGAGTGTAAAGCTCTGAGGGTTTATGACAGGGCTTGTACAGCGAG 390
QY 361 ATCTTTTGCATATCCCTGTGACATGACAGGATCCTGGCCATTTGCTCAATGCTGTGTT 420
DB 391 ATCTTTTGCATATCCCTGTGACATGACAGGATCCTGGCCATTTGCTCAATGCTGTGTT 450
QY 421 GCCCTTGAGGCCGGAAGCTGCTCTTTTGTGTGTATGACAGGATCCTGACCTGGGCGCTG 480
DB 451 GCCCTTGAGGCCGGAAGCTGCTCTTTTGTGTGTATGACAGGATCCTGACCTGGGCGCTG 510
QY 481 GGAAGTCTGAGGCTCTCTCTGAAATTTATCTTATGAGCTGAAAGGTTGTAAAGAG 540
DB 511 GGAAGTCTGAGGCTCTCTCTGAAATTTATCTTATGAGCTGAAAGGTTGTAAAGAG 570
QY 541 ACTCTTTGAGGCTCTCTTTTACCAAGAGATACAGTATATAGCTGAGGCGATTTTCCACT 600
DB 571 ACTCTTTGAGGCTCTCTTTTACCAAGAGATACAGTATATAGCTGAGGCGATTTTCCACT 630
QY 601 CTGAGATGACCAATCTTGTGTGTCTGCTCTGCTGTGCTGTTATGGCCATCTGTACACA 660
DB 631 CTGAGATGACCAATCTTGTGTGTCTGCTCTGCTGTGCTGTTATGGCCATCTGTACACA 690
QY 661 GGAATCATGAAAGCGTGTGAGGTCGCCAGTAAAAAGTAAAGGCAAGGCGATCCGGCTC 720
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QY 721 ATTTTGTGATCAATGAGCGGTGTTTCAATTTCTGACACCTTACATGTGCTATCTT 780
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QY 781 CTCTCTTCTTATCAATTCATCTTATTTTGAATGACTGTGAGCGGAGCAATCTTGAC 840
DB 811 CTCTCTTCTTATCAATTCATCTTATTTTGAATGACTGTGAGCGGAGCAATCTTGAC 870
QY 841 CTGCTATGCTGTGACAGAGGATGCTTCTTCCACCTGCTGACAGTAAACCGGATGATC 900
DB 871 CTGCTATGCTGTGACAGAGGATGCTTCTTCCACCTGCTGACAGTAAACCGGATGATC 930
QY 901 TACGCTTTTGTGAGAGAGGTTCCGGAAGTACCTTGCGCACTTCTTCCACAGGCACTTG 960
DB 931 TACGCTTTTGTGAGAGAGGTTCCGGAAGTACCTTGCGCACTTCTTCCACAGGCACTTG 990
QY 961 CTGATGACCTGTGGCGAGATACATCCCATCTTCTTCTATGTAAGAGCTGAAAAACAGC 1020
DB 991 CTGATGACCTGTGGCGAGATACATCCCATCTTCTTCTATGTAAGAGCTGAAAAACAGC 1050
QY 1021 TCTGTCTCTCAATCCAGAGAGCGGGAAGCTCTTATGTGTGTT 1065
DB 1051 TCTGTCTCTCAATCCAGAGAGCGGGAAGCTCTTATGTGTGTT 1095

RESULT 2
CN837388 867 bp mRNA linear EST 02-JUN-2004
LOCUS AGENCOURT.15864186 NIH_MGC.145 Homo sapiens cDNA clone
DEFINITION IMAGE:7001957 3', mRNA sequence.
ACCESSION CN837388
VERSION CN837388.1 GI:47943043
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgs@nih-mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Place: IRB13 row: c column: 03
High quality sequence stop: 708.
Location/Qualifiers
1. 867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7001957"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_1lb="NIH MGC 145"
/note="Vector: pCDNA3.1. Site 1: varies by clone; site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-ScorV-XbaI/XhoI-3',
5'-ScorV-XbaI/NotI-3', 5'-ScorV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/featuring/plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."
ORIGIN
Query Match 78.4%; Score 835; DB 7; Length 867;
Best Local Similarity 99.1%; Pred. No. 3,1e-230;
Matches 849; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 ATGACAACCTCACTAGATACAGTTGAGACCTTGGTACCAATCTTACTATGATGACGTG 60
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QY 61 GGGCTGCTCTGTGAAAAAGCTGATACCAAGACCTGATGCGCCAGTTTGGCCCCGCTG 120
DB 71 GGGCTGCTCTGTGAAAAAGCTGATACCAAGACCTGATGCGCCAGTTTGGCCCCGCTG 130
QY 121 TACTCCCTGTGTGCTGTGGGCGCTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 131 TACTCCCTGTGTGCTGTGGGCGCTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGT 190
QY 181 AATAACAGAGGCTCCGAATTATGACCAATCTTACTGCTCAACCTGGCCATTTGCGAC 240
DB 191 AATAACAGAGGCTCCGAATTATGACCAATCTTACTGCTCAACCTGGCCATTTGCGAC 250
QY 241 CTGCTCTTCTGTGCAACCTTCCATTTCTGATTCCTATGTCCAGGGGCGATTACTGGGTT 300

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Db 251 CGCTCTTCTGTCACCTTCATCTGAGATCACTATGTCAGGGGGCATTAACGAGT 310
Qy 301 TTTGGCAGAGGAGTGTAAAGCTCTTCAGAGGTTTATCAGAGGCTTGTACAGCGAG 360
Db 311 TTTGGCAGAGGAGTGTAAAGCTCTTCAGAGGTTTATCAGAGGCTTGTACAGCGAG 370
Qy 361 ATCTTTTCAATATCTGCTGACAAATGACAGAGTCTGGCCATGTTCCATGCTGTTT 420
Db 371 ATCTTTTCAATATCTGCTGACAAATGACAGAGTCTGGCCATGTTCCATGCTGTTT 430
Qy 421 GCCCTTGCAGCCCGGACCTGTCATCTTTGGTGTATCAGCAGATCTGTCACCTGGAGCCTG 480
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Qy 481 GCAAGTGTAGAGAGCTCTTCTGTAATTTATCTTATGAGATGAGAGTGTGTAAGAG 540
Db 491 GCAAGTGTAGAGAGCTCTTCTGTAATTTATCTTATGAGATGAGAGTGTGTAAGAG 550
Qy 541 ACTCTTTGAGAGTCTTTTACCCAGAGATAGATATATAGCTGAGAGCATTTCCACACT 600
Db 551 ACTCTTTGAGAGTCTTTTACCCAGAGATAGATATATAGCTGAGAGCATTTCCACACT 610
Qy 601 CTGAGAAATGACCATCTTCTGTCCTGTTCTCCCTGCTGCTGTTATGAGCATCTGCTACACA 660
Db 611 CTGAGAAATGACCATCTTCTGTCCTGTTCTCCCTGCTGCTGTTATGAGCATCTGCTACACA 670
Qy 661 GGAATATCAAAACGCTGCTGAGTGCCCGCAATAAAAAAGTACAGGCAATCCGGCTC 720
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Qy 721 ATTTTGTATCATGAGCGGT-GTTTTTCAATTTTCTGAGACACCTCAATAGTGGTATCT 779
Db 731 ATTTTGTATCATGAGCGGTGTTTTTCAATTTTCTGAGACACCTCAATAGTGGTATCT 790
Qy 780 TCTCTCTTCTATCATCATCTTATTTGGAATGATGCTGAGCGGAGCAACATCTGGA 839
Db 791 TCTCTCTTCTATCATCATCTTATTTGGAATGATGCTGAGCGGAGCAACATCTGGA 850
Qy 840 CCGGTATGCTGTGCA 856
Db 851 CCGGTATGCTGTGNTA 867

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RESULT 3
CN801748 1002 bp mRNA linear EST 26-MAY-2004
LOCUS ILUMIGEN MCQ 35976 Katze MMP1 Macaca mulatta cDNA clone
DEFINITION ILUMIGEN MCQ 35976 Katze MMP1 Macaca mulatta cDNA clone
CDS (Hs.506190), mRNA sequence.
ACCESSION CN801748
VERSION CN801748.1 GI:47697724
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 1002)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL PUBMED
Genome Biol. 6 (7), R60 (2005)
1598449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780408
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.11. 688 Q20 bases.

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PCR Primers
FORWARD: CCTCATTAAGGAGAACAAA
BACKWARD: CACTATAGGGCAATGGGTA.
Insert Length: 1002 Std Error: 0.00
Plate: G4000213 row: B column: 03
Seq primer: CCTCATTAAGGAGAACAAA
POLYA=No.

FEATURES
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Location/Qualifiers
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/sex="female"
/dev_stage="newborn infant"
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/clone_lib="Katze_MMP1"
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I; Site 2: Xho I; Created from StrataGene ZAP-cDNA
Synthesis kit (catalog #200400) and ZAP-cDNA GigaPack III
Gold Cloning Kit (catalog #200450)"

ORIGIN
Query Match 76.7%; Score 816.4; DB 7; Length 1002;
Best Local Similarity 90.1%; Pred. No. 8e-225;
Matches 896; Conservative 0; Mismatches 96; Indels 2; Gaps 2;

Qy 73 GAAAAAGCTGATACAGAGCACTGATGAGGCGCATTTGTCCTGTTGCTGCTGCTG 132
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Qy 133 TTCATGAGGAGCTCTGAGGAGATGAGTGTGAGTGTGATGATCTCTAATAATACAGAG 192
Db 61 TTCATGAGGAGCTCTGAGGAGATGAGTGTGAGTGTGATGATCTCTAATAATACAGAG 120
Qy 193 CTCGGAATATGACCAACATCTACCTGCTCAACTGAGCCATTTGGAACCTGCTCTC 252
Db 121 CTCGGAATATGACCAACATCTACCTGCTCAACTGAGCCATTTGGAACCTGCTCTC 180
Qy 253 GTCACCTTTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
Db 181 TTCACCTTTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Qy 313 ATGTGTAGAGCTCTCTGAGGAGTTTATACACAGGCTGTACAGGAGATCTTTTAT 372
Db 241 ATGTGTAGAGCTCTCTGAGGAGTTTATACACAGGCTGTGTACAGGAGATCTTTTAT 300
Qy 373 ATCTGTGACCAATGACAGATGATGATGATGATGATGATGATGATGATGATGATG 432
Db 301 ATCTGTGACCAATGACAGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 433 CGGACTGTCACTTTTGTGTATGACAGGATGATGATGATGATGATGATGATGATGAT 492
Db 361 AGGACTGTCACTTTTGTGTATGACAGGATGATGATGATGATGATGATGATGATGAT 420
Qy 493 GCTCTTCTGATTTTATCTTATGAGATGAGAGTGTGTAAGAGCTCTTGTGAGT 552
Db 421 GCTCTTCTGATTTTATCTTATGAGATGAGAGTGTGTAAGAGCTCTTGTGAGT 480
Qy 553 GCTCTTACCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 612
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Qy 613 ATCTTCTGCTGTTCTCTCTCTGCTGCTGATGAGCCATGCTGTACACAGGAATCAT 672
Db 541 ATCTTGTCTGCTCTCTCTCTCTGCTGCTGATGAGCCATGCTGTACACAGGAATCAT 600
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Qy 733 ATGGGAGGTGTTTCAATTTTCTGACACCTCAATGATGAGTATGCTTCTCTCTAT 792

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Db 661 ATGGCTGATGTTTCTATTTCTGACACCCCTACATGAGGCTATCTTACTCTAT 720
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Qy 853 GTGACAGAGTGATGCGCTACTCTCCACTGCTGCATGAAACCCGGATATCTACCCCTTTGT 912
Db 781 GCGAGCGAAGGATTTCCCTACTCCCACTGCTGCATGAAACCC-GTATCTAACCCCTTTGT 839
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Qy 973 GGCAGATATCATCCCATTTCTCTCTAGTGAAGACT-GAAAGAACAGCTGTCTCTCC 1031
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Db 960 CTCCACAGCAAAACCCGAAATCTTTTGTGTTT 993

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RESULT 4
CN837645/c 793 bp mRNA linear EST 02-JUN-2004
LOCUS AGENCOURT 15669744 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:7001957 5', mRNA sequence.
ACCESSION CN837645.1 GI:47943300
VERSION EST.
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgnabs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
http://image.llnl.gov
Plate: IRB13 row: c column: 03
High quality sequence scop: 649.
Location/Qualifiers

FEATURES

source

1. 793
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:7001957"
/issue_type="mixed"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_145"
/notes="Vector: pCDNA3.1; Site 1: varied by clone; Site 2:
varied by clone; ORFs were PCR-emplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmaI/XhoI-3',
5'-EcoRV-XmaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1_presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 784; DB 7; Length 793;
Best Local Similarity 99.4%; Pred. No. 1.8e-215;
Matches 787; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 274 CACTATGTGAGGGGAGCATTAAGTGGTTTGGCCATGCGATGTAAGTCTCTCTCAGGG 333
Db 793 CACTATGTGAGGGGAGCATTAAGTGGTTTGGCCATGCGATGTAAGTCTCTCTCAGGG 734
Qy 334 TTTTATCAACAGGCTTTGACAGGAGATCTTTTATTAATCTGCTGACATGACAGG 393
Db 733 TTTTATCAACAGGCTTTGACAGGAGATCTTTTATTAATCTGCTGACATGACAGG 674
Qy 394 TACCTGGCATTTGTCATGCTGTGTTTCCCTTCAGGCCGAGCTGTCACTTTTGTGTC 453
Db 673 TACCTGGCATTTGTCATGCTGTGTTTCCCTTCAGGCCGAGCTGTCACTTTTGTGTC 614
Qy 454 ATACACAGCATGTCACCTGAGGCTGTGAGAGAGCTTTGACAGGATTTATCTTC 513
Db 613 ATACACAGCATGTCACCTGAGGCTGTGAGAGAGCTTTGACAGGATTTATCTTC 554
Qy 514 TATGAGCTGAAGAGTTGTTGAAGAGCTTTGACAGGATTTATCTTC 573
Db 553 TATGAGCTGAAGAGTTGTTGAAGAGCTTTGACAGGATTTATCTTC 494
Qy 574 GTATATGACTGAGGATTTTCACTGTAAGATGACATCTTCTGTCTGTTCTCCCT 633
Db 493 GTATATGACTGAGGATTTTCACTGTAAGATGACATCTTCTGTCTGTTCTCCCT 434
Qy 634 CTGCTGTTATGAGGATCTGCTACACAGGAATCATCAAAAGCTGTGAGGTCCTCCAGT 693
Db 433 CTGCTGTTATGAGGATCTGCTACACAGGAATCATCAAAAGCTGTGAGGTCCTCCAGT 374
Qy 694 AAAAAAAGTCAAGGAGCATCCGCTCATTTTGTGATCATAGGCGGTGTTTCAATTTTC 753
Db 373 AAAAAAAGTCAAGGAGCATCCGCTCATTTTGTGATCATAGGCGGTGTTTCAATTTTC 314
Qy 754 TGGACACCTTCAATATGAGTATCTTCTCTCTCTATTCATTCATCTTATTTGAAAT 813
Db 313 TGGACACCTTCAATATGAGTATCTTCTCTCTCTATTCATTCATCTTATTTGAAAT 254
Qy 814 GACTGTGAGCGGAGCAAGCATCTGCACTGTGTATGCTGTGACAGAGTATCCCTTAC 873
Db 253 GACTGTGAGCGGAGCAAGCATCTGCACTGTGTATGCTGTGACAGAGTATCCCTTAC 194
Qy 874 TCCCATGCTGTGATGAACCCGGTATCTAAGCCTTTGTTGAGAGAGGTTCCGAAATAC 933
Db 193 TCCCATGCTGTGATGAACCCGGTATCTAAGCCTTTGTTGAGAGAGGTTCCGAAATAC 134
Qy 934 CTGCGCACTTCTTCCACAGGCACTTGTCTATGCACTGTGGAGATATATCCCATTTCTT 993
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Qy 994 CTTAGTGAAGAGCTGAAAAGAAACAGCTGTGTCTCTCATTCACAGCAGAGCCGAACTTC 1053
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RESULT 5
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DEFINITION BG205056 Aherysys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG205056
VERSION BG205056.1 GI:13726743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 789)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 521.
Location/Qualifiers
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/cell_line="HT1080"
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/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 70.3%; Score 748.8; DB 2; Length 789;
Best Local Similarity 98.6%; Pred. No. 2.9e-205;
Matches 764; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
1 ATGAAACCTCACTGATATACATGAGACCTTGGTACCAATCTTACTATATATGACCTG 60
16 ATGAAACCTCACTGATATACATGAGACCTTGGTACCAATCTTACTATATATGACCTG 75
61 GGCCTGCTCTGTGAAAAAGCTGATACAGAGACATGATGAGGAGGAGGAGGAGGAGGAG 120
76 GGCCTGCTCTGTGAAAAAGCTGATACAGAGACATGATGAGGAGGAGGAGGAGGAGGAG 135
121 TACTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
136 TACTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 195
181 AAATACAGAGGCTCCGAAATATGACCAATCTTACTGCTTACCTGAGGAGGAGGAGGAGGAG 240
196 AAATACAGAGGCTCCGAAATATGACCAATCTTACTGCTTACCTGAGGAGGAGGAGGAGGAG 255
241 CTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
256 CTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
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316 TTGGCCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
381 ATCTTTTTCATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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496 GGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 555

541 ACTCTTTCAGAGGCTCTTTACCCAGAGATATATATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
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601 CTGAGAAATGACATCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 660
616 CTGAGAAATGACATCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 675
661 GGAATCATCAAAAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
676 GGAATCATCAAAAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 735
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RESULT 6
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DEFINITION BG182330
ACCESSION BG182330
VERSION BG182330.1 GI:13704017
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 884)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
JOURNAL PUBLISHED
COMMENT Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atherys.com
High quality sequence stop: 529.
Location/Qualifiers
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/cell_line="HT1080"
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/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
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Best Local Similarity 98.3%; Pred. No. 7.2e-195;
Matches 742; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
1 ATGAAACCTCACTGATATACATGAGACCTTGGTACCAATCTTACTATATATGACCTG 60
17 ATGAAACCTCACTGATATACATGAGACCTTGGTACCAATCTTACTATATATGACCTG 76
61 GGCCTGCTCTGTGAAAAAGCTGATACAGAGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
77 GGCCTGCTCTGTGAAAAAGCTGATACAGAGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 136

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Db		197	AAATACAGAGAGGCTCCGAATTATGACCAACATCTAACCTGGCCATTTCGGAC	256
Oy		241	CTGCTCTTCTCTGTCAACCCTTCCATTCTGTGANTCCATATGTGCAGGGGGCATACTGGGTT	300
Db		257	CTGCTCTTCTCTGTCAACCCTTCCATTCTGTGANTCCATATGTGCAGGGGGCATACTGGGTT	316
Oy		301	TTTGGGACATGGCATTGTGTAAGCTCCCTGCAGGGGTTTTATACACAGGCTTGTACAGCGAG	360
Db		317	TTTGGGACATGGCATTGTGTAAGCTCCCTGCAGGGGTTTTATACACAGGCTTGTACAGCGAG	376
Oy		361	ATCTTTTTCATPATCTCTGTGACCAATGCAGAGTACCTGGCCATTGTTCATGCTGTGTTT	420
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Oy		481	GCAGTGTACAGAGCTCTTCTGAATTATTTCTTCTATAGACTGAAGAATTGTTGAAGAG	540
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DEFINITION	603063322P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212541 5',	mRNA sequence.		
ACCESSION	B1906283			
VERSION	B1906283.1	GI:16168946		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	1 (bases 1 to 876)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nhl.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: The Life Technologies, Inc. CNDA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.jiml.gov Plate: LIML1533 row: k column: 06			

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                non-activated adult donors. Library is oligo-dT primed
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                cloning). Average insert size 1.7 kb, insert size range
                1.2-3.3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Grubbs
                (Invitrogen). Research Genetics tracking code 027. Note:
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ORIGIN

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Best Local Similarity	97.2%	Pred. No. 3.4e-192		
Matches 769; Conservative	0	Mismatches 17	Indels 5	Gaps 5

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Db	139	GGCCTGCTCTGTAAGAAAAGCTGATACAGAGCACTGATGCGCCAGTTTGTGCCCCGCTG	198
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Db	259	AAATACAGGAGGCTCCGAATTATGACCAACATCTACCTGCAACTGACCAATTCGAC	318
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Db	319	CTGCTCTTCTGTGCAACCTTTCATTTCTGATCCATATGTGAGGGGCATTAATCTGGATT	378
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Oy	481	GCGAGTCTGAGAGCTCTTCTCTGAA-TTTATCTCTCAATGAGCTGAAGAGTTGTTGAAG	538
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Oy	540	GACTCTTTCGAGGCTCTTTATCCGAGAGATACAGTATATAGCTGAGGCAATTTCCACAC	598
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Oy	659	CAGGAATCATAAAAAGCTGTGAGAGTGCCCAAGTAAAAAAAGTACA-AGGCAATCCGG	717
Db	738	CAGGAATCATAAAAAGCTGTGAGAGTGCCCAAGTAAAAAAAGTACAGTCAAGCAATCCGG	797

QY 718 CTCATTTTTCATGATGCGGCTGTTTTCATTTTCTGACACCCCTACATGNGGCTATC 777
 DB 798 CTCATTTTTCGCGCATATGCGGCGG-TAACCATTTTCTGACACCCCTACATGNGGCTATC 856
 QY 778 CTTCTCTCTTC 788
 DB 857 CTTCTCTATTC 867

RESULT 8
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 DEFINITION AGSC00RT 30842869 NIH MGC_146 Homo sapiens cDNA clone
 IMAGE:7385709 5', mRNA sequence.
 ACCESSION CO960092.1 GI:51324665
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 702)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bbs-rmml.nih.gov
 Tissue Procurement: Guthrie cDNA Resource Center
 cDNA Library Preparation: Guthrie cDNA Resource Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILML at:
 http://image.llnl.gov
 Place: IRB17 row: c column: 11
 High quality sequence start: 26
 High quality sequence stop: 538.
 Location/Qualifiers

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 from commercially available cDNA libraries) and cloned by
 the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
 into pCDNA3.1. For specific information on cloning sites
 (which vary by clone), please refer to the Guthrie
 website, using the Guthrie ID given in the file
 ftp://image.llnl.gov/image/rearrayed_plates/IRBF.presv.dat
 a. Note: this is a NIH_MGC library."

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 Query Match 64.0%; Score 681.4; DB 7; Length 702;
 Best Local Similarity 98.4%; Pred. No. 9,7e-186;
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 DB 63 GGCCTGCTCTGTGAAAAGCTGATACAGAGCACTGATGAGCCAGTTTGTCCCGCTG 122

QY 121 TACTCCCTGCTGTTCACTGTGGGCTCTTTGGCAATGTGGTGTGTGATGATTCCTCAT 180
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 QY 241 CTTCTCTCTGCTGACCCCTTCATCTGATTCACATGTCAGAGGCGCATTAATGAGTT 300
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 QY 301 TTGTCAGATGCGATGTAAAGCTCTCTCAGGCTTTATACACAGGCTTTGACAGCG 360
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 QY 361 ATCTTTTCATATCTGCTGACCAATTCAGAGGTAACCTGGCCATTTGCTGCTGTT 420
 DB 363 ATCTTTTCATATCTGCTGACCAATTCAGAGGTAACCTGGCCATTTGCTGCTGTT 422
 QY 421 GCCCTTCCAGCCCGAGCTGTCACTTTGGTGTATCACAGGATGCTGAGGCGCTG 480
 DB 423 GCCCTTCCAGCCCGAGCTGTCACTTTGGTGTATCACAGGATGCTGAGGCGCTG 482
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 DB 603 CTGAAATGACATCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
 QY 661 GGAATCATCAAAAGCTGCTGAGGAGGCGCCAGTAAAAA 699
 DB 663 GGAATCATCAAAAGCTGCTGAGGAGGCGCCAGTAAAAA 701

RESULT 9
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 DEFINITION 9286 Full length cDNA from the Mammalian Gene Collection Homo
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 ACCESSION CV030237
 VERSION CV030237.1 GI:51488473
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 675)
 Rual, J.F., Hirozane-Kleishkawa, T., Hao, T., Bertin, N., Li, S.,
 Driscoll, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,
 Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,
 Stimson, B., Sequerra, R., Bosak, G., Doucette-Stamm, L., Le Peuch, C.,
 Vandenhaute, J., Cusick, M.E., Alcala, J.S., Hill, D.B. and Vidal, M.
 Human ORFome Version 1.1: a Platform for Reverse Proteomics
 Genome Res. (2004) In press
 Contract: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, Boston, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc_Vidal@dfci.harvard.edu
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
 results from a PCR reaction using an MGC full-length cDNA as
 template DNA and ORF specific primers
 PCR Primers

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

4
11076861

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

5
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

6
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2284)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, O., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numata, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/RRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers

FEATURES
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Best Local Similarity 76.6%; Pred. No. 1.7e-177;
Matches 800; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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2284
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22 GTTAGACCTTTGGTACCACTCTCTATGATGACGTGGCTGCTCTGAAAAAGCT 81
248 GTTGAACCTTTGAGACCAACCCATGAAATGATGATGGGACCAACCCCTGGAAAAATGC 307
82 GATACCAAGACATGATGGCCCAAGTTTGGCCCCGCTGTACTCCCTGGTGTCACTGG 141
308 AGAATCAAGAGCTGGGATCATGCTCTGCTCCACTGATCTCTGTGTATCATC 367
142 GGCCTCTGGGCAATGTGTGGTGTGATGATCTCATATAAATACAGAGGCTCCGAAT 201
368 GGCCTCTGGGCAATATGTTGTGTGATTCCTCATATAAGTACAGAGCTACAAAT 427
202 ATGACCAATCTACCTGCTCACTGCTGCAATTTGGACCTGCTTCTCTGACCTT 261
428 ATGGTATATCTACTCTGTCACACTTGGCAATTTCTGACCTGCTTCTCTGACCTTC 487
262 CCATTCGATTCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 321
488 CCATTCGATTCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
322 CTCCTGAGGCTTTTATACACAGGCTTTGACAGGAGATCTTTTATATCTGCTG 381
548 ATGCTGTGGGTTTATTAATCTGCTTTGACAGGAGATCTTTTATATCTGCTG 607
382 ACAATGACAGTACCTGCTGCAATGTCATGCTGTGTTTCCCTTGGAGCCGGAATGTC 441
608 ACAATGACAGTACCTGCTGCAATGTCATGCTGTGTTTCCCTTGGAGCCGGAATGTC 667
442 ACTTTGATGATACAGAGATGCTGACCTGAGGCTGAGAGCTGAGCTTCTCT 501
668 ACTTTGATGATACAGAGATGCTGACCTGAGGCTGAGAGCTGAGCTTCTCT 727
502 GAATTTATCTGATGACATGAGGCTTTGAAAGAGACTTTTGAAGTCTCTTAC 561
728 GAATTTATCTGATGACATGAGGCTTTGAAAGAGACTTTTGAAGTCTCTTAC 787
562 CCAAGAGATACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621
788 CCAAGAGATACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
622 CTCGTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
848 CTAGCTCTTCT 907
682 AGGTGCCCCAGTAAAAAAGTAAAGGAGCATCCGGCTCATTTTGTGATCATGCGGTG 741
908 AATATGCCAATAAAAAAGTAAAGGAGCATCCGGCTCATTTTGTGATCATGCGGTG 967
742 TTTTTCATTTTGTGACACCTCAATGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 801
968 TTTTTCATTTTGTGACACCTCAATGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1027
802 TTTTTCATTTTGTGACACCTCAATGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 861
1028 TTTTTCATTTTGTGACACCTCAATGATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
862 GTGATGCTTATCCCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 921
1088 GTGATGCTTATCCCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1147

QY 922 TTCGGAGTACCTGCGCACTTCTTCCACAGGCACTTGCTCATGCACTGGGCGAGATAC 981
 Db 1148 TTCGGAGAACACCTTCGGCTCTTTTCCACAGAAATGCGCAGTTTACTCGGAGAAATAT 1207
 QY 982 ATCCCATTCCTTCTAGTAGAGAGAGCTGGAAGAACCAAGCTGTCTCTTCATCCACAGCA 1041
 Db 1208 ATTCGTTTCTTCTCTGTGAGAAATGAGAAAGAACAGCTGTCTCCCATCACTGAG 1267
 QY 1042 GAGCCGGAACCTCTCTATGTGTTT 1065
 Db 1268 GAGCAAGAAATCTGTGTGTGTTT 1291

RESULT 12
 AK089895
 LOCUS
 DEFINITION Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830047J12 product: chemokine (C-C) receptor 3, full insert sequence.
 ACCESSION AK089895.1 GI:26354724
 VERSION AK089895.1
 KEYWORDS HTG; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Buteleyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 JOURNAL High-efficiency full-length cDNA cloning
 PubMed Meth. Enzymol. 303, 19-44 (1999)
 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 PubMed Genome Res. 10 (10), 1617-1630 (2000)
 11042159

TITLE
 JOURNAL The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 PubMed Functional annotation of a full-length mouse cDNA collection
 Authors Nature 409, 685-690 (2001)
 5

TITLE
 JOURNAL The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 PubMed Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Authors Nature 420, 563-573 (2002)
 6 (bases 1 to 2396)

REFERENCE
 AUTHORS Fukuda, S., Hayatsu, N., Hiramoto, K., Hiraka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Kato, S., Kono, H., Konda, M., Kato, H., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, D., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

JOURNAL
 TITLE
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome-gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 URL: http://location.qualifiers

FEATURES
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ORIGIN
 Query Match 61.4%; Score 653.6; DB 4; Length 2396;
 Best Local Similarity 76.6%; Pred. No. 1.7e-177;
 Matches 800; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

QY 22 GTTGAACCTTGGTACCACTCTATATATATGAGCGGCGCTGCTGTAAGAAAGCT 81
 Db 119 GTTGAAGCTTGGACCAACACCTTATATATATGAGCGGCGCAACCTGTAAGAAAGCT 178
 QY 82 GATACCAAGCACTGATGCGCCAGTTTGTGCCCCGCTGTACTCCCTGGTGTCACTGTG 141
 Db 179 AGAATCAAGAGCTGGGATCAAGGCTCTGCTTCACTGATCTCCCTGGTGTCACTATC 238
 QY 142 GGCCTCTGGGCAATGTGTGTGTATATATCTCATATTAATAAGAGAGGTCGGAAT 201
 Db 239 GGCCTCTGGGCAATATATGTGTGTGTATATCTCATATTAAGTACAGAGAGCTACAAAT 298
 QY 202 ATGACCAATCTACTCTGCACTGCGCAATTTGCACTGCTCTCTGCTGCACTCT 261
 Db 239 ATGCTATATCTACTCTGCACTGCGCAATTTGCACTGCTCTCTCTGCTGCTG 358
 QY 262 CCATCTGATTCACATATGTCAGGGGCAATACCTGGTTTGGCGCAGGCAATGTATAG 321
 Db 359 CCATCTGATTCACATATGTTCTGTGGAATGATGTGGGCTTTGGCCACTGATGTGCAAA 418

QY 322 CTCTCTGAGGGTTTATTCACAGAGCTGTGACAGAGATCTTTTCAATCTCTGCTG 381
DB 419 ATGCTGTGGGTTTATTAACCTGGCTGTGACAGAGATCTTTTCAATCTCTGCTG 478
QY 382 ACAATGACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
DB 479 ACAATGACAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
QY 442 ACTTTTGGTGTATCAGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501
DB 539 ACTTTTGGTGTATCAGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
QY 502 GAATTTATCTTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 561
DB 599 GAATTTATCTTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 658
QY 552 CCAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 621
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QY 622 CTGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
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QY 682 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
DB 779 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 838
QY 742 TTTTTCATTTTCTGAGACCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 801
DB 839 TTTTTCATTTTCTGAGACCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 898
QY 802 TTTTTCATTTTCTGAGACCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 861
DB 899 TTTTTCATTTTCTGAGACCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 958
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DB 959 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
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DB 1019 TTTTTCATTTTCTGAGACCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1078
QY 982 ATCCCATCTTCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1041
DB 1079 ATCCCATCTTCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1138
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RESULT 13
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LOCUS RST3417 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.
DEFINITION BG204024
ACCESSION BG204024
VERSION BG204024.1 GI:13725711
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 745)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Bozzer, S.,
Mayer, R., Smith, B., Veloso, N., Kika, A., Hess, J., Cochran, K., Lo, K.,
Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random

JOURNAL activation of gene expression
PUBMED Nat. Biotechnol. 19 (5), 440-445 (2001)
COMMENT 11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 447.
Location/Qualifiers
1..745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_id="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 61.2%; Score 651.6; DB 2; Length 745;
Best Local Similarity 95.7%; Pred. No. 4.3e-177;
Matches 691; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

QY 10 TCACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 69
DB 16 TCACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 75
QY 70 TGTGAAAAAGTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 129
DB 76 TGTGAAAAAGTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 135
QY 130 GTTTCATCTGAGGCTCTGAGGCAATGATGATGATGATGATGATGATGATGATGATGATG 189
DB 136 GTTTCATCTGAGGCTCTGAGGCAATGATGATGATGATGATGATGATGATGATGATGATG 195
QY 190 AGGCTCCGAATATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 249
DB 196 AGGCTCCGAATATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 255
QY 250 CTGTCACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 309
DB 256 CTGTCACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 315
QY 310 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 369
DB 316 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 375
QY 370 ATATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 429
DB 376 ATATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 435
QY 430 GCCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489
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QY 490 GCAAGCTCTT-CTGAAATTTATCTTATGAGATGAGATGAGATGAGATGAGATGAGATGAG 548
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QY 549 CAGTGTCTTTTACCGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 608
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QY 728 TGC 729
DB 736 CC 737

RESULT 14
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LOCUS Homo sapiens CCR1 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY399291
VERSION AY399291.1 GI:39755280
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1086)
AUTHORS Clark,A.G., Gdanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeilio,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1086)
AUTHORS Clark,A.G., Gdanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeilio,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN
Query Match 50.8%; Score 540.8; DB 10; Length 1086;
Best Local Similarity 69.3%; Pred. No. 6.5e-145;
Matches 737; Conservative 0; Mismatches 327; Indels 0; Gaps 0;

QY 1 ATGAACCTCACTGATGATGACCTTGTGATCCATCTTACTATGATGACG 60
DB 19 ATGAACCTCACTGATGATGACCTTGTGATCCATCTTACTATGATGACG 78
QY 61 GGCCTGCTCTGTGAAAAAGCTGATACAGAGCACTGATGAGCCAGTTGTGCCCCGCTG 120
DB 79 GCAACTCCGTCGCAAGAGTGAACAGAGGCGCTTTGGGGCCCACTGCTGCCCCCTG 138
QY 121 TACTCCCTGCTGATCACTGTGGGCTCTTGGGCAATGTGGTGTGATGATCTCTATA 180
DB 139 TACTCCCTGCTGATCACTGTGGGCTCTTGGGCAATGTGGTGTGATGATCTCTATA 198
QY 181 AATATAGAGAGGCTCGAATATATGACCAATCTACTCTCAACCTGAGCATTTGCGAC 240
DB 199 CATTACAGAGGCTATAAATACATGACCAATCTACTCTCTTAACCTGAGCATTTCTGAC 258
QY 241 CTGCTCTTCTCTGTCACCTTCATCTTGATTCATATGTCAGGGGGCATTAATGAGGTT 300

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QY 301 TTGGCCATGAGAGTGTGATGATGATCTCTCTCAAGGTTTATCACAGAGCTTGTACAGCAG 360
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QY 361 ATCTTTTCATATCTCTGTGACCAATTCAGAGATCTTGGCATTTGTCCATCTGTGTT 420
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QY 421 GCCCTTCAGAGCCGGAATCTCTTTGTGTCATCAACAGATGTCACCTGGGCGCTG 480
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QY 481 GCAAGTCTAGAGCTCTCTCTGATTTTATCTTATGAGATCGAAGATGTTGTAAG 540
DB 499 GCCATCTGGCTTCCATGTCAGAGCTTATATCTTTCCAGAGCCATTTGGAATTCATCAG 558
QY 541 ACTCTTGTAGTCTCTTTTACCCAGAGATACAGTATATAGCTGAGGCAATTTCCACT 600
DB 559 CACACCTGAGGCTTCACTTTCTTCAAGAAAGCTTACAGAGATGAGCTGTTTCAAGCT 618
QY 601 CTGAAATGACCATTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 619 CTGAAATGACCATTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
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QY 841 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 859 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
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DB 919 TACGCTTGTGTGAGAGAGGTTCCGAAATACCTGCGCACTTCTTCCACAGAGGCTG 978
QY 961 CTGATGACCTGTGAGAGATCAATCCATCTCTCTTCTGATGAGAGCTGAGAAACAGC 1020
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DB 1039 TCCACATCTCTCTTCCAGAGGAGATCAATCTCTGCTGAGTT 1082

RESULT 15
CR609171 2583 bp mRNA linear HTC 21-JUL-2004
LOCUS Full-length cDNA clone CS0D1086YK1 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR609171
VERSION CR609171.1 GI:50489978
KEYWORDS HTC; cNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 2583)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 2583)
Genoscope.
Direct Submission
Submitted (20-Jul-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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/clone="CSOD108YK11"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

COMMENT

COMMENT

FEATURES

source

1..2583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD108YK11"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 50.8%; Score 540.8; DB 4; Length 2583;
Best Local Similarity 69.3%; Pred. No. 8.6e-145;
Matches 737; Conservative 0; Mismatches 327; Indels 0; Gaps 0;

QY 1 ATGACACCTGCTAGTACAGTGTGAGACCTTGGTACACACCTGATATGATGACG 60
DB 19 ATGGAACCTCCAAACACACAGAGAGCTATGACACACACAGATTGATCATAGG 78
QY 61 GGCCTGCTCTGTGAAAAAGCTGATACAGAGACCTGATGAGCCAGTTTGCCCGCTG 120
DB 79 GGAACCTCGGTGCAAGAGGTGAACAGAGAGGCTTTGGGGCCCACTGCTGCCCTCTG 138
QY 121 TACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 139 TACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 198
QY 181 AAATCAGAGAGCTCCGATTTATGACCAATCTACCTGCTGACCTGAGCACTTGGAC 240
DB 199 CAATACAGAGAGCTAAACCAATGACCAATCTACCTGCTGACCTGAGCACTTGGAC 258
QY 241 CTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 259 CTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
QY 301 TTGGCCATGCAATGTGTAAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 319 TTGGGTATGCAATGTGTAAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378
QY 361 ATCTTTTATATATCTGCTGCAATGCAATGCAATGCAATGCAATGCAATGCTGCT 420
DB 379 ATCTTTTATATATCTGCTGCAATGCAATGCAATGCAATGCAATGCAATGCTGCT 438
QY 421 GCCCTTGAAGCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 439 GCTTGGGGGCAAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
QY 481 GCAATGCTGCAAGCTCTCTGCAATTTATCTGATGAGCTGAAGAGTTTGAAGAG 540
DB 499 GCAATGCTGCTGCAAGCTCTCTGCAATTTATCTTTCAGAGCCCAATGGGAATCACT 558
QY 541 ACTCTTTGAGAGCTCTTATCCAGAGATACAGATATAGCTGAGGAGCACTTCCAC 600
DB 559 CACACTGAGAGCTTCTCTCAAGAGCTTCAAGAGCTTCAAGAGCTTCTCTCAAGGCT 618
QY 601 CTGAGATGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 619 CTGAAATGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
QY 661 GGAATCATAAAGCTGCTGAGAGTCCCAATGAAAAAGTACAGGCAATCCGCTC 720

DB 679 GGAATTAATAAGATTCTCTAAGACACCAATGAAAGAAATCCAAAGCTGCTGTTG 738
QY 721 ATTTTGTATCATAGCCGCTGTTTTCATTTTCTGAGACCCCTTACATATGCTATCTT 780
DB 739 ATTTTGTATCATATGATCATCTTTTCTCTTTTGAACCCCTTACATTTGATATCTT 798
QY 781 CTCTTCTTCTATCATCATCTTATTTGAAATGACTGTGAGCCGAGAGCATTTGAGC 840
DB 799 ATTTCTGTTTCCAGACTTCTGTTCAACCATGATGTGAGCAGAGACATTTGAGC 858
QY 841 CTGATCATCTGAGAGAGAGGTGATGCTTACTCCACTGCTGATGACCCGCTGATC 900
DB 859 CTGCTGCAAGTATGAGAGGTATCCCTTACAGCACTGCTGTGTACACCACTGATC 918
QY 901 TACGCTTGTGTGAGAGAGGTTCGGAAGTACCTGCGCACTTCTTCAAGGACCTTG 960
DB 919 TACGCTTGTGTGAGAGGTTCGGAAGTACCTGCGCACTTCTTCAAGGACCTTG 978
QY 961 CTGATCATCTGAGAGAGGTATGCTTCTTCTGATGAGAGAGTGAAGAACCAAGC 1020
DB 979 GCTGTGCACTGCTGTTAAATGCTCCCTCTCTCCGAGACAGGCTGAGAGGCTCAGC 1038
QY 1021 TCTGTCTGCTTCCATCCAGAGAGCCGGAATCTCTATTTGCTT 1064
DB 1039 TCCATATCTCTCTCCAGAGAGGAGCATGAACTCTTCTGCTGCTT 1082

Search completed: January 7, 2006, 19:14:03
Job time : 3890.92 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 07:05:07 ; Search time 83.4673 Seconds
(without alignments)
3912.475 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	448	100.0	1945	US-11-127-877-27	Sequence 27, Appli
3	41	9.2	2908	US-10-793-626-4359	Sequence 4359, Ap
4	40.8	9.1	10467	US-10-240-708-2	Sequence 2, Appli
5	40.4	9.0	6070	US-10-240-708-10	Sequence 10, Appli
6	40.4	9.0	151169	US-11-121-086-38	Sequence 38, Appli
7	40.2	9.0	151169	US-11-121-086-38	Sequence 38, Appli
8	40	8.9	4765	US-10-750-185-64847	Sequence 64847, A
9	40	8.9	4765	US-10-750-185-64847	Sequence 64847, A
10	39	8.7	157230	US-11-112-908-64	Sequence 64, Appli
11	39	8.7	166111	US-11-112-908-47	Sequence 64, Appli
12	39	8.7	170508	US-11-112-908-62	Sequence 62, Appli
13	39	8.7	173115	US-11-112-908-65	Sequence 65, Appli
14	38.8	8.7	6306	US-10-240-708-49	Sequence 49, Appli
15	37.6	8.4	201	US-10-995-561-60497	Sequence 60497, A
16	37.6	8.4	68123	US-10-995-561-13348	Sequence 13348, A
17	37.2	8.3	5278	US-10-750-185-61034	Sequence 61034, A
18	37.2	8.3	5278	US-10-750-623-61034	Sequence 61034, A
19	37	8.3	2655	US-10-793-626-1659	Sequence 1659, Ap
20	37	8.3	3520	US-10-793-626-4160	Sequence 4160, Ap
21	36.8	8.3	158692	US-11-121-086-30	Sequence 30, Appli
22	36.8	8.2	2076	US-10-750-185-27635	Sequence 27635, A
23	36.8	8.2	2076	US-10-750-623-27635	Sequence 27635, A

24	36.8	8.2	1080000	US-10-928-446A-1	Sequence 1, Appli
25	36.8	8.2	1080000	US-10-928-446A-181	Sequence 181, App
26	36.8	8.2	1080000	US-10-928-446A-183	Sequence 183, App
27	36.8	8.2	1080000	US-10-928-446A-185	Sequence 185, App
28	36.8	8.2	1080000	US-10-928-446A-187	Sequence 187, App
29	36.8	8.2	1080000	US-10-928-446A-189	Sequence 189, App
30	36.8	8.2	1080000	US-10-928-446A-191	Sequence 191, App
31	36.8	8.2	1080000	US-10-928-446A-193	Sequence 193, App
32	36.8	8.2	1080000	US-10-928-446A-195	Sequence 195, App
33	36.8	8.2	1080000	US-10-928-446A-197	Sequence 197, App
34	36.8	8.2	1080000	US-10-928-446A-199	Sequence 199, App
35	36.8	8.2	1080000	US-10-928-446A-201	Sequence 201, App
36	36.6	8.2	207908	US-11-112-908-21	Sequence 21, Appli
37	36.6	8.2	212805	US-11-112-908-19	Sequence 19, Appli
38	36.6	8.2	1082144	US-11-117-187-211	Sequence 211, App
39	36.4	8.1	2286	US-10-750-185-60490	Sequence 60490, A
40	36.4	8.1	2286	US-10-750-623-60490	Sequence 60490, A
41	36.4	8.1	48000	US-11-159-597-20	Sequence 20, Appli
42	36.2	8.1	5152	US-10-240-708-73	Sequence 73, Appli
43	36.2	8.1	110711	US-10-995-561-13264	Sequence 13264, A
44	36	8.0	175416	US-11-121-086-43	Sequence 43, Appli
45	35.8	8.0	1691140	US-11-091-018-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-068-686-3
; Sequence 3, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Report, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/068,686
FILING DATE: 28-Feb-2005
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 362..1426
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88-28 polynucleotide and amino acid


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; Sequence 2, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-240-708-2

Query Match          9.1%; Score 40.8; DB 6; Length 10467;
Best Local Similarity 5.5%; Pred. No. 0.83;
Matches 69; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      317 TAAACCTTTATTTATTTATACCTTACGCGAGCTATGATATATAAAACATT 376
Db      3763 TTAACATTATATATCTCTAATATATCCCAATATAAATATAATATATACATT 3724

Qy      377 TCACCATACATAGTAACTATTTTCTTAATGCTGCTTCTTCCCT 432
Db      3723 TAAAAAATAAATACTACGACGATATACTCATATATCCCAACT 3668

; RESULT 5
; US-10-240-708-10/C
; Sequence 10, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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; US-10-240-708-10
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Best Local Similarity 5.1%; Pred. No. 0.86;
Matches 95; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy      207 ACTCATATCAACCTTAAGGACAGGCTTCTCTCTTAAGAGTACTTACA 266
Db      2774 AATTATATCTTTTCAAAATCTCATTTAATTAATTAATTAATCTTACATT 2715

Qy      267 TTTTAATGACCTGAATGTTAGTACTATATGCGCTACAAAAGTAAACCTTT 326
Db      2714 TTTTAAATCTAATATATATTAATTAATTAATTAATTTCTTCAATTAATTA 2655

Qy      327 TATATTTATACATTAACCTGACGAGCTATGATATAATTAACATTTTCACACATA 386
Db      2654 TAAATTAACATTAATTTATATATATTAATTAATTAATTAATTAATTTTCCCTTAA 2595

Qy      387 CAATTA 392
Db      2594 CTATTA 2589

; RESULT 6
; US-11-121-086-38
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-38

Query Match          9.0%; Score 40.4; DB 7; Length 151169;
Best Local Similarity 5.3%; Pred. No. 2.8; 71; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy      243 TCTCTTAAATGAGTACTACATTTTAATGCACTGAAAGTTAGATGTTACTATANG 302
Db      47401 TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 47460

Qy      303 CCGCTACAAAAGGTAAACCTTTTATATTTTATACATTACTTACGCGAGCTATGATA 362
Db      47461 ATATATATATATATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTA 47520

Qy      363 TAAATTAACATTTTCACACATACATTAAGTTA 396
Db      47521 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 47554

; RESULT 7
; US-11-121-086-38/C
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
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QY 280 GAATGTAGATAGTACTATATATGCGCTACAAAAGTAAACCTTTTATATTTATACA 339
DB 125173 GAAGTTGAGGTTATTAACATGAGAGAGTCACTGAATTTAAATCTTTAGACCTTAAAA 125114
QY 340 TTAACCTGAGCCAGCTATTGATATATAATTAACATTTTCACAAATACATTAAGTTACT 399
DB 125113 TTACATTTGAGCAAAACCAAGATGAGAGAAAATATTGCAAACTAAATTTAGTTTAAAT 125054
QY 400 ATTTAATTTTCTAATGTCCTAG 422
DB 125053 ATTTAATTAAGAAATTAAGCAAG 125031

RESULT 11

US-11-112-908-47
; Sequence 47, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 166111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-47

Query Match 8.7%; Score 39; DB 7; Length 166111;
Best Local Similarity 48.8%; Pred. No. 6.5;
Matches 105; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 234 CTTTCTCTCTCTCTAAATGAGTTACTTATGACCTGAATGTAAATACT 293
DB 151045 CTTTCTCTCTCTCTAAATGAGTTACTTATGACCTGAATGTAAATACT 151104
QY 234 TACTATATGAGCGCTCAAAAAGTAAACCTTTTATATTTTATACATTAAGTTACT 353
DB 151105 TACTATGCTCCATTAATCAATTTTGTCTATTAATTTTGTCAATACACCTGCTGATTAAT 151164
QY 354 CTATGATTAATAATAAATTAATTTTCAACATTAATTAAGTTAACTAATTTTCTTAA 413
DB 151165 GTATGTAAGTCTACATTTGAGTAGCGTCAAGTCCCTGACCTTGTGCTTTGTTGGTG 151224
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DB 151225 TTAATCTGAGTCTTTTGTGCTCCATGTAACCTT 151259

RESULT 12

US-11-112-908-62/c
; Sequence 62, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 170508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-62

Query Match 8.7%; Score 39; DB 7; Length 170508;
Best Local Similarity 54.5%; Pred. No. 6.6;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 280 GAATGTAGATAGTACTATATATGCGCTACAAAAGTAAACCTTTTATATTTATACA 339
DB 108929 GAAGTTGAGGTTATTAACATGAGAGAGTCACTGAATTTAAATCTTTAGACCTTAAAA 108870
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DB 108869 TTACATTTGAGCAAAACCAAGATGAGAGAAAATATTGCAAACTAAATTTAGTTTAAAT 108810
QY 400 ATTTAATTTTCTAATGTCCTAG 422
DB 108809 ATTTAATTAAGAAATTAAGCAAG 108787

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US-11-112-908-65/c
; Sequence 65, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 173115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-65

Query Match 8.7%; Score 39; DB 7; Length 173115;
Best Local Similarity 54.5%; Pred. No. 6.6;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 280 GAATGTAGATAGTACTATATATGCGCTACAAAAGTAAACCTTTTATATTTATACA 339
DB 60684 GAAGTTGAGGTTATTAACATGAGAGAGTCACTGAATTTAAATCTTTAGACCTTAAAA 60625
QY 340 TTAACCTGAGCCAGCTATTGATATATAATTAACATTTTCACAAATACATTAAGTTACT 399
DB 60624 TTACATTTGAGCAAAACCAAGATGAGAGAAAATATTGCAAACTAAATTTAGTTTAAAT 60565
QY 400 ATTTAATTTTCTAATGTCCTAG 422

GenCore version 5.1.6
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Title: US-10-767-521-4

Perfect score: 448
Sequence: 1 tagctcagatgcagaagaatt.....ccctgcttaatgaaagctt 448

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	448	100.0	448	8	US-10-767-521-4
3	448	100.0	1717	3	US-09-964-824A-100
4	448	100.0	1717	7	US-10-641-643-905
5	448	100.0	1717	5	US-10-843-641A-5403
6	448	100.0	1915	5	US-10-106-623-3
7	448	100.0	1915	8	US-10-772-037-3
8	448	100.0	5791	9	US-10-929-182-21
9	448	100.0	5791	9	US-10-486-471-5
10	380.4	84.9	1689	3	US-09-931-381A-15
11	380.4	84.9	1689	6	US-10-283-028-1
12	339.2	75.7	7201	6	US-10-311-455-310
13	294.4	65.7	7201	6	US-10-311-455-309
14	105	23.4	600	10	US-11-060-756-2216
15	105	23.4	600	10	US-11-060-756-2216
16	105	23.4	1201	5	US-10-225-567A-63
17	105	23.4	1201	6	US-10-305-720-1085
18	105	23.4	1201	7	US-10-641-643-905
19	105	23.4	1201	6	US-10-988-257-5
20	50	11.2	50	6	US-10-131-827-2200
21	48.4	10.8	3673778	6	US-10-312-841-2
22	46.8	10.4	7025	7	US-10-257-166-142
23	46.8	10.4	7025	7	US-10-240-454-46

C 24	45.4	10.1	3673778	6	US-10-312-841-1	Sequence 1, Appl1
C 25	44	9.8	731	4	US-09-925-065A-934088	Sequence 934088,
C 26	43	9.6	650	5	US-10-027-632-231715	Sequence 231715,
C 27	43	9.6	650	5	US-10-027-632-231716	Sequence 231716,
C 28	43	9.6	650	5	US-10-027-632-231717	Sequence 231717,
C 29	43	9.6	650	6	US-10-027-632-231715	Sequence 231715,
C 30	43	9.6	650	6	US-10-027-632-231716	Sequence 231716,
C 31	43	9.6	650	6	US-10-027-632-231717	Sequence 231717,
C 32	43	9.6	3025	5	US-10-027-632-258968	Sequence 258968,
C 33	43	9.6	3025	5	US-10-027-632-258970	Sequence 258970,
C 34	43	9.6	3025	5	US-10-027-632-258971	Sequence 258971,
C 35	43	9.6	3025	6	US-10-027-632-258968	Sequence 258968,
C 36	43	9.6	3025	6	US-10-027-632-258970	Sequence 258970,
C 37	43	9.6	3025	6	US-10-027-632-258971	Sequence 258971,
C 38	42.8	9.6	731	4	US-09-925-065A-934087	Sequence 934087,
C 39	42.8	9.6	731	4	US-09-925-065A-934089	Sequence 934089,
C 40	42.6	9.5	3025	5	US-10-027-632-258969	Sequence 258969,
C 41	42.6	9.5	3025	6	US-10-027-632-258969	Sequence 258969,
C 42	42.2	9.4	2865	7	US-10-221-714A-42	Sequence 42, Appl1
C 43	42.2	9.4	5269	6	US-10-311-455-2029	Sequence 2029, Ap
C 44	42.2	9.4	9905	6	US-10-311-455-36	Sequence 36, Appl1
C 45	42	9.4	595	4	US-09-925-065A-605996	Sequence 605996,

ALIGNMENTS

RESULT 1
US-09-922-895-4
; Sequence 4, Application US/09922895
; Publication No. US20020192214A1
; GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
DEPARTMENT, UTILS A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL ROTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Metrick & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,895
FILING DATE: 06-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/847,296
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19634Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-922-895-4

Query Match 100.0%; Score 448; DB 3; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.5e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 60
DB 1 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 60
OY 61 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 120
DB 61 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 120
OY 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 180
DB 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 180
OY 181 ACCAAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTTGCT 240
DB 181 ACCAAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTTGCT 240
OY 241 TCTCTCTCTAAATGATTAAGTACCTTAATGACCTGAATGTTAGATGTTACTATA 300
DB 241 TCTCTCTCTAAATGATTAAGTACCTTAATGACCTGAATGTTAGATGTTACTATA 300
OY 301 TGCCTCTACAAAAGGTAAAGCTTTTATATATTAACATTAACCTGACCGCTATTGA 360
DB 301 TGCCTCTACAAAAGGTAAAGCTTTTATATATTAACATTAACCTGACCGCTATTGA 360
OY 361 TATAATATAAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 420
DB 361 TATAATATAAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 420
OY 421 AGTCTCTTCCCTGCTTAATGAAAAGCTT 448
DB 421 AGTCTCTTCCCTGCTTAATGAAAAGCTT 448
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RESULT 2
US-10-767-521-4
Sequence 4, Application US/10767521
Publication No. US2005003024A1
GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: DEMARTINO, JULIE A.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SPRINGER, MARTIN J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING EOSINOPHIL EOTAXIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 19634YDCA
CURRENT APPLICATION NUMBER: US/10/767,521
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: 60/016,158
PRIOR FILING DATE: 1996-04-26
PRIOR APPLICATION NUMBER: 09/922,895
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 448
TYPE: DNA
ORGANISM: Human
US-10-767-521-4

Query Match 100.0%; Score 448; DB 8; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.5e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 60

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DB 1 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 60
OY 61 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 120
DB 61 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 120
OY 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 180
DB 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 180
OY 181 ACCAAGGCGAGGGGCTGGGAGCGTACTCATCAACCTTAAGAGAGCTTTGCT 240
DB 181 ACCAAGGCGAGGGGCTGGGAGCGTACTCATCAACCTTAAGAGAGCTTTGCT 240
OY 241 TCTCTCTCTAAATGATTAAGTACCTTAATGACCTGAATGTTAGATGTTACTATA 300
DB 241 TCTCTCTCTAAATGATTAAGTACCTTAATGACCTGAATGTTAGATGTTACTATA 300
OY 301 TGCCTCTACAAAAGGTAAAGCTTTTATATATTAACATTAACCTGACCGCTATTGA 360
DB 301 TGCCTCTACAAAAGGTAAAGCTTTTATATATTAACATTAACCTGACCGCTATTGA 360
OY 361 TATAATATAAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 420
DB 361 TATAATATAAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 420
OY 421 AGTCTCTTCCCTGCTTAATGAAAAGCTT 448
DB 421 AGTCTCTTCCCTGCTTAATGAAAAGCTT 448
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RESULT 3
US-09-964-824A-100
Sequence 100, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO 100
LENGTH: 1717
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-100

Query Match 100.0%; Score 448; DB 3; Length 1717;
Best Local Similarity 100.0%; Pred. No. 7.9e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 60
DB 1270 TAGGTCAATGCAAGAAATTCCTTAAGAGAGACCAAGAGATGAAGCAACACTT 1329
OY 61 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 120
DB 1330 AAGCTTCCACACTCACTCTTAAGACAGTCTTCAAGTCAACCTGAAGCTC 1389
OY 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 180
DB 1390 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACCTTAAGTCAAT 1449
OY 181 ACCAAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTTGCT 240
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Query Match	100.0%	Score 448;	DB 7;	Length 1717;
Best Local Similarity	100.0%;	Pred. No. 7.9e-100;		
Matches 448; Conservative	0;	Mismatches	0;	Gaps 0

TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-5403


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? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (4015)..(5082)
? OTHER INFORMATION:
? PUBLICATION INFORMATION:
? DATABASE ACCESSION NUMBER: GenBank AF247361
? DATABASE ENTRY DATE: 2002-06-26
? RELEVANT RESIDUES: (1)..(5791)
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US-10-466-471-5

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Query Match	100.0%;	Score 448;	DB 9;	Length 5791;
Best Local Similarity	100.0%;	Pred. No. 1.3e-9;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	TAGGCAATCAGAAAATTCCTTAAAGAGAAAGACCAAGAGATGAAGAAACAATT	60
Db	5080	TAGTCAGATCAGAAAATTCCTTAAAGAGAAAGACCAAGAGATGAAGAAACAATT	5139
OY	61	AAGCTTCACACTCACTCTPAAAAGTCCTTCAACTTCCAGTGCACAACCTGAAGCTC	120
Db	5140	AAGCTTCACAACCTCACTCTPAAAAGTCCTTCAACTTCCAGTGCACAACCTGAAGCTC	5199
OY	121	TTGAAGACACTGAAATATACACAGCAGTAGAGATAGATGATGATCCCTAAGGCTATT	180
Db	5200	TTGAAGACACTGAAATATACACAGCAGTAGAGATAGATGATGATCCCTAAGGCTATT	5259
OY	181	ACCAAGGCGCAGGGGCTGGGCGAGCTACTCATCAACCTTAAAAAGCAGAGCTTTGCT	240
Db	5260	ACCAAGGCGCAGGGGCTGGGCGAGCTACTCATCAACCTTAAAAAGCAGAGCTTTGCT	5319
OY	241	TCTCTCTCTTAAATATAGTTACTCTACATTTTATGACCTGAAATGTTAATAGTTACTATA	300
Db	5320	TCTCTCTCTTAAATATAGTTACTCTACATTTTATGACCTGAAATGTTAATAGTTACTATA	5379
OY	301	TGCGCGTCAAAAAAGTAAACCTTTTATATTTTATACATTAACTTCAGCAGCATATGA	360
Db	5380	TGCGCGTCAAAAAAGTAAACCTTTTATATTTTATACATTAACTTCAGCAGCATATGA	5439
OY	361	TATAAATAAAACAATTTTCAACAATATACATAAGTAACTATTTTATTTTCTAATGTGCTT	420
Db	5440	TATAAATAAAACAATTTTCAACAATATACATAAGTAACTATTTTATTTTCTAATGTGCTT	5499
OY	421	AGTCTCTTCCCGCTTAATGAAGAACTT 448	
Db	5500	AGTCTCTTCCCGCTTAATGAAGAACTT 5527	

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/ RESULT 10
/ US-09-931-381A-15
/ Sequence 15, Application US/09931381A
/ Patent No. US20020137107A1
/ GENERAL INFORMATION:
/ APPLICANT: Butcher, Eugene C.
/ APPLICANT: Kunkel, Eric J.
/ APPLICANT: Pan, Junliang
/ APPLICANT: Soler-Ferran, Dulce
/ TITLE OF INVENTION: Method for Identifying Agents Which
/ TITLE OF INVENTION: Modulate Chemokine "Mec"-Induced Functions of CCR3 and/or
/ TITLE OF INVENTION: CCR10
/ FILE REFERENCE: 1855.2010-003
/ CURRENT APPLICATION NUMBER: US/09/931,381A
/ CURRENT FILING DATE: 2001-08-15
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: U.S. 09/638,914
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15
/ LENGTH: 1689
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
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; NAME/KEY: CDS
; LOCATION: (181) ... (1248)
; NAME/KEY: misc feature
; LOCATION: (1291) ... (1291)
; OTHER INFORMATION: n = A, T, C or G
US-09-931-381A-15

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Query Match	84.9%;	Score 380.4;	DB 3;	Length 1689;
Best Local Similarity	98.4%;	Pred. No. 3.4e-83;		
Matches 436;	Conservative 0;	Mismatches 2;	Indels 5;	Gaps 5

OY	7	GGATGCGAAAATATGGCTTAAGAGGAAGAACCAAGATGAGCAACACATTAAGCT	66
Db	1251	AGATGCGAAAATATGGCTTAAGAGGAAGAACCAAGATGAGCAACATTAAGCT	1311
OY	67	TCCACTCAGCCTCTAANAAGTCTTCAA-CTTCAGTGCACACTGAAAGCTTTGAA	125
Db	1311	TCCACTCAGCCTCTAANAAGTCTTCAA-CTTCAGTGCACACTGAAAGCTTT- AA	1366
OY	126	GACACTGAAATATATCACACAGCAGTAGAGATGATGATGATACCTTAAGTCAATACAC	185
Db	1370	GACACTGAAATATATCACACAGCAGTAGAGATGATGATGATACCTTAAGTCAATACAC	1422
OY	186	AGGCGAGGGGCTGGGCAAGCTACTCATCATCAACCTTAANAAGCAGAGCTTGTCTCT	245
Db	1430	AGGCGCA-GGGCTGGGGCAGCTACTCATCATCAA-CTTAANAAGCAGAGCTTGTCTCT	1487
OY	246	CTCTTAATATGATTAACCTTCAATTTTAAGCACTGAAAGTTAGATGATTAACATATAGCGG	305
Db	1488	CTCTTAATATGATTAACCTTCAATTTTAAGCACTGAAAGTTAGATGATTAACATATAGCGG	154
OY	306	CTACAAAAGGTAAAACTTTTATATTTTATATACATTAACCTCAGCAGCTATATGATATA	365
Db	1548	CTACAAAAGGTAAAACTTTTATATTTTATATATTAACATTAACCTCAGCAGCTATAT-ATAATA	1600
OY	366	ATPAAAACATTTTCACACATACATATAAGTTAATAATTTTATTTTCTAATGTGCTTAGTTC	425
Db	1607	ATPAAAACATTTTCACACATACATATAAGTTAATAATTTTATTTTCTAATGTGCTTAGTTC	1667
OY	426	TTTCCCTGCTTAATGAAAAGCTT 448	
Db	1667	TTTCCCTGCTTAATGAAAAGCTT 1689	

RESULT 11
 US-10-283-028-1
 Sequence 1, Application US/10283028
 Publication No. US20030143684A1
 GENERAL INFORMATION:
 APPLICANT: Gerard, Craig J.
 Gerard, No. US20030143684A1ma P.
 Mackay, Charles R.
 Ponath, Paul D.
 Post, Theodore W.
 Qin, Shixin
 TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
 ANTAGONISTS THEREOF
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Millitia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/283,028
 FILING DATE: 28-Oct-2002

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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 310
LENGTH: 7201
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-310

Query Match          75.7%; Score 33912; DB 6; Length 7201;
Best Local Similarity 84.8%; Pred. No. 8,8e-73;
Matches 380; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      1 TAGGTCAGATGACGAAAAATTGCTTAAAGAGAGAACCAAGAGATGACGAAACACTT 60
DB      1105 TAATCAAAATACAAAAAATTACCTTAAAAAACAACAAAAAATTAACCAACACTT 1046

QY      61 AAGCTTCCGACTGCTGCTTAAACAGTCTTCAAACTTCCAGTGCAGACGAAAGCTC 120
DB      1045 AAACCTTCCGACTGCTGCTTAAACAGTCTTCAAACTTCCAGTGCAGACGAAAGCTC 986

QY      121 TTGAAGACACTGAAATTAACACAGAGATGAGATGATGATGATGATGATGATGAT 180
DB      985 TTAAAAACACTTAAATTAACACAGACATTAACATTAATTAATTAATTAATTAAT 926

QY      181 ACCACAGGCCGAGGCGCTGGCGAGCTATCATCAACCTTAAAAAGCAGAGCTTGT 240
DB      925 ACCACAAACGAAAAAAGCTAAACAAAGTACTGATGACCTTAAAAAAGAACTTACT 866

QY      241 TCTCTCTTAAAAATGAGTTACCTTAACTTTTAATGACACTGAAATGATGATGATGAT 300
DB      865 TCTCTCTTAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 806

QY      301 TGGCGTACGAAAAAGGTAACCTTTTAACTTTTAACTTAATTAATTAATTAATTA 360
DB      805 TACCGTACGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 746

QY      361 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB      745 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 686

QY      421 AGTTCCTTCCCTGCTTAAATGAAGCTT 448
DB      685 AATTCCTTCCCTACTTAAATAAAAACTT 658

RESULT 13
US-10-311-455-309
Sequence 309, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PLEBENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
TITLE OF INVENTION: cyclosporine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01

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NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 309
; LENGTH: 7201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATRE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-309

Query Match 65.7%; Score 294.4; DB 6; Length 7201;
Best Local Similarity 78.6%; Pred. No. 9.4e-62;
Matches 352; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 60
DB 6097 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 6156
QY 61 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 120
DB 6157 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 6216
QY 121 TTGAAGACACTGAAATATACACAGAGATGAGATGATGATGATGATGATGATGAT 180
DB 6217 TTGAAGATATGAAATATATATATATATATATATATATATATATATATATAT 6276
QY 181 ACCACAGCCAGGCGCTGGGACGCTACTCATCATCAACCTTAAGAGAGAGCTT 240
DB 6277 ATTATAGTGTAGGGGTGGGTAGCGTATTTATTTAAAGTGAAGTGTGTT 6336
QY 241 TCTCTCTAAATGATGATACCTACATTTTAAGACCTGAAGTGAATGATGATGAT 300
DB 6337 TTTTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6396
QY 301 TCCCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTAT 360
DB 6397 TCTCGTAAATAAGGTAAATTTTATATTTTATATATATTTTATAGTATGAT 6456
QY 361 TATTAATTAATTAATTTTCAACATAATTAATTAATTTTATTTTCTAAATGCT 420
DB 6457 TATTAATTAATTAATTTTATATATTAATTAATTAATTTTATTTTATATGTT 6516
QY 421 AGTTCCTTCCCTCTTAATGAAGCTT 448
DB 6517 AGTTCCTTCCCTCTTAATGAAGCTT 6544

RESULT 14

US-11-060-756-2216
; Sequence 2216, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2216
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2216

Query Match 23.4%; Score 105; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 60
DB 496 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 555

QY 61 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 105
DB 556 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 600

RESULT 15

US-11-060-756-6488
; Sequence 6488, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6488
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-6488

Query Match 23.4%; Score 105; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 60
DB 496 TAGGTCAAGTGCAGAAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 555
QY 61 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 105
DB 556 AAGCTTCACACTGACCTCTTAAGAGAGAGCAAGAGATGAAGCAACACTT 600

Search completed: January 7, 2006, 20:31:33
Job time : 330.171 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:45:42 ; Search time 1634.64 Seconds
(without alignments)
12822.754 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448

Sequence: 1 tagctcagatcgacgaatac.....ccctgctatcgaaagctt 448

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: gb_est3:*
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7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	159.6	35.6	640	7	CK953877 4093669 B
C 3	154.8	34.6	498	6	CB476821 jns12 E03
C 4	154.6	34.5	652	6	CF368588 853245 MA
C 5	154.6	34.5	683	7	CN153669 940808 MA
C 6	143.2	32.0	649	7	CK948708 4073860 B
C 7	134.6	30.0	475	11	CR922120 Sus scrofa
C 8	134.6	30.0	723	11	CR922142 Sus scrofa
C 9	105.6	23.6	1761	4	AK041106 Mus muscu
C 10	105.6	23.6	2396	4	AK089895 Mus muscu
C 11	93	20.8	2284	4	AK089875 Mus muscu
C 12	76.4	17.1	655	2	BB223728
C 13	75	15.8	632	6	CF367184 841909 MA
C 14	71	15.0	657	7	CO683220 Dg11-166f
C 15	67	15.0	832	7	CN155784 943112 MA
C 16	65.6	14.6	274	2	BF553209 UT-R-C2-n
C 17	49.4	11.0	320	2	BB25464 BB25464
C 18	49.4	11.0	1079	1	AJ927148 AJ927148
C 19	47.4	10.6	1203	10	CNS015WU
C 20	47.2	10.5	687	3	BP179101
C 21	47.2	10.5	939	9	CC223760
C 22	47.2	10.5	1027	10	CNS02750

23	47.2	10.5	1034	9	CC206179
24	47.2	10.5	1086	9	CC258597
C 25	46.4	10.4	1101	10	CNS016L1
C 26	46.2	10.3	421	10	CE644562
C 27	46.2	10.3	726	10	CZ668371
C 28	46.2	10.3	914	10	CNS002J7
C 29	46	10.3	1101	10	CNS0172Q
C 30	45.8	10.2	975	10	CNS0102Y
C 31	45.2	10.1	883	2	BG603853
C 32	44.6	10.0	874	9	AZ541515
C 33	44.6	10.0	1027	10	CNS02750
C 34	44.4	9.9	1205	10	CNS0165A
C 35	44.4	9.9	1341	10	AG430330
C 36	44.2	9.9	681	3	BP178582
C 37	44.2	9.9	829	9	BH501921
C 38	44.2	9.9	987	10	CNS014PO
C 39	44.2	9.9	1101	10	CNS0106X
C 40	44	9.8	938	6	CD050219
C 41	43.6	9.7	342	3	BP733312
C 42	43.6	9.7	538	1	AJ625164
C 43	43.6	9.7	699	9	AQ323327
C 44	43.6	9.7	771	10	AG539796
C 45	43.6	9.7	1052	10	AG520832

ALIGNMENTS

RESULT 1
BG220110/c 747 bp mRNA linear EST 21-APR-2001
LOCUS RST39882 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG220110
ACCESSION BG220110
VERSION BG220110.1 GI:13746131
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 747)
Harrington,J., J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McMilligott, K., Boozar, S., Mays, R., Smith, B., Veloso, N., Klitz, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence atp: 523.
Location/Qualifiers
1..747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 86.5%; Score 387.4; DB 2; Length 747;

Best Local Similarity 98.5%; Pred. No. 4,5e-84;
Matches 391; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 1 TAGGTCAGATGAGAGAAATTCCTTAAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGATTT 60
DB 403 TAGGTCAGATGAGAGAGAAATTCCTTAAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGATTT 344
OY 61 AAGCTTCACACCTCACTCACTTAAACAGTCTTCAAACTTCCAGTGCACACCTGAGCTC 120
DB 343 AAGCTTCACACCTCACTCACTTAAACAGTCTTCAAACTTCCAGTGCACACCTGAGCTC 284
OY 121 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 180
DB 283 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 224
OY 181 ACCAAGGCGAGGGGCTGGGCGAGCTACATCATCATCAACCTTAAAGAGAGAGCTTTGCT 240
DB 223 ACCAAGGCGAGGGGCTGGGCGAGCTACATCATCATCAACCTTAAAGAGAGAGCTTTGCT 164
OY 241 TCTCTCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 300
DB 163 TCTCTCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 104
OY 301 TGCCGCTACAAAAGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 360
DB 103 TGCCGCTACAAAAGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 44
OY 361 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 397
DB 43 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7
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RESULT 2
CK953877/c 640 bp mRNA linear EST 15-MAR-2004
LOCUS DEFINITION 4093669 BARC 10BOV Bos taurus CDNA clone 10BOV32_H12 3', mRNA
sequence.
ACCESSION CK953877
VERSION CK953877.1 GI:45468257
KEYWORDS EST
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, W. and Gasbarre, L.C.
TITLE Production of EST from CDNA libraries derived from immunologically activated bovine gut

JOURNAL
COMMENT Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tade@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim faesa. Vector identified
by cross match using options -mismatch 12 -mismatch 18
Plate: 32 row: H column: 12
Seg primer: AGCGATACATTCATTCACACAGG
High quality sequence stop: 640.
Location/Qualifiers

FEATURES
source

1..640
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV32_H12"
/sex="Male"
/issue_type="Pooled"

/dev_stage="Multiple"
/lab_host="D10B T1 phage resistant"
/clone_id="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site: 1;
ECORV; Site 2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

Query Match 35.6%; Score 159.6; DB 7; Length 640;
Best Local Similarity 73.4%; Pred. No. 2.6e-28;
Matches 279; Conservative 0; Mismatches 79; Indels 22; Gaps 5;

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OY 1 TAGGTCAGATGAGAGAAATTCCTTAAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGATTT 60
DB 375 TAGGTCAGATGAGAGAAATTCCTTAAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGATTT 316
OY 61 AAGCTTCACACCTCACTCACTTAAACAGTCTTCAAACTTCCAGTGCACACCTGAGCTC 119
DB 315 G-----ACCTCTTCAACAGTCTTCAAACTTCCAGTGCACACCTGAGCTC 270
OY 120 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 179
DB 269 TTGAAGACACTGAATATATACACAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 210
OY 180 TACCAAGGCGAGGGGCTGGGCGAGCTACATCATCATCAACCTTAAAGAGAGAGCTTTGCT 239
DB 209 TACCAAGGCGAGGGGCTGGGCGAGCTACATCATCATCAACCTTAAAGAGAGAGCTTTGCT 151
OY 240 TCTCTCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 299
DB 150 TCTCTCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 96
OY 300 ATGCGGCTACAAAAGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 359
DB 95 ATGCGGCTACAAAAGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAAATGATTAACCTTAA 37
OY 360 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 379
DB 36 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 17
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RESULT 3
CB476821/c 498 bp mRNA linear EST 26-MAR-2003
LOCUS DEFINITION jne12.803.f jns Sus scrofa CDNA f', mRNA sequence.
ACCESSION CB476821
VERSION CB476821.1 GI:29283207
KEYWORDS EST
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Buktayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleostomi; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

1 (bases 1 to 498)
Title Sequence analysis of African swine fever virus infected and
non-infected porcine macrophage CDNA libraries
Unpublished (2003)
Contact: Neilan JG
Plum Island Animal Disease Center
US Department of Agriculture, Agricultural Research Service
PO Box 848, Greenvale, NY 11944-848, USA
Tel: 631 323 3133
Fax: 631 323 3044
Email: jneilan@plad.cars.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.020425.c and
trimmed with the aid of the trim alt option. Vector identified by
cross match v0.990329 and Lucy vl.17p.
Seq primer: M13 Forward
Location/Qualifiers

FEATURES

SOURCE

1. 498
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="lymphoid"
/cell_type="macrophage"
/lab_host="DH10B"
/clone_1ib="jns"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI;
Library made from pools of polyA selected RNA. Macrophages
were derived from peripheral blood mononuclear cells
cultured for 48 hrs on plastic in the presence of 30% L929
supernatant."

ORIGIN

Query Match 34.6%; Score 154.8; DB 6; Length 498;
Best Local Similarity 73.6%; Pred. No. 3.7e-27;
Matches 281; Conservative 0; Mismatches 87; Indels 14; Gaps 6;
QY 29 AGAAGACCAAGAGATGAGCAACACATTAAAGCTTCCACACTCCTCTAAACAG 88
DB AGTCAGATGCAAGAACATTGTTGAGAGATGAGCAAAATACATTGACCTCTATACAG 311
QY 89 TCCCTCAACTCCAGTGCACACTGAAAGCTCTGAAAGCACTGAAATATACACAGCA 148
DB 310 TCCCTGAACTTCCAGCAGACAGCTGAAGCT-TTGAAGACATTAAATATATACCAATG 252
QY 149 GTAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 208
DB 251 GTGAGGATATATCTATGACCCCAAGTCATTAACCAAGTCATGATGATGATGATG 193
QY 209 TCATCATCAAGCTTAAAGAGAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 268
DB 192 TCGTGTCACCTGAGAGAGAGAGCTTGTCTGATTCCTCA--GAGTTACATACATT 135
QY 269 TTAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
DB 134 TTAATGACCTGAA-GTATGATGATGATGATGATGATGATGATGATGATGATGAT 76
QY 329 TATTTATATCATTAATCTTCCAGCAGCTATGATATATATATATATATATATAT 387
DB 75 TCTTTT-----ACTTCAGCCAGTATATGACATTAAGAAACATATTTCAAAATAC 24
QY 388 AATAAGTTAATCTATTTT 409
DB 23 AATAATGATTAATCTCTTT 2

RESULT 4

CF368588 652 bp mRNA linear EST 25-AUG-2003
LOCUS DEFINITION 853245 MARC 3P1G Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CF368588
VERSION CF368588.1 GI:34174248
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 652)
AUTHORS Smith,T.P.L., Preking,B.A., Ford,J.J., Valliet,J.L., Fox,J.,
Wise,T.A., Noneman,D.J., Wray,J.R. and Keefe,J.W.
TITLE A second set of porcine ESTs from a pooled-tissue normalized
library
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_aln option. Vector identified with
cross match v0.990329.
Plate: SRG8025 row: I column: 17
Seq primer: TAGAAGGACAGTCAGG.
Location/Qualifiers

FEATURES

SOURCE

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/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 3P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

ORIGIN

Query Match 34.5%; Score 154.6; DB 6; Length 652;
Best Local Similarity 74.0%; Pred. No. 4.3e-27;
Matches 279; Conservative 0; Mismatches 84; Indels 14; Gaps 6;
QY 29 AGAAGACCAAGAGATGAGCAACACATTAAAGCTTCCACACTCCTCTAAACAG 88
DB 375 AGTCAGATGCAAGAACATTGTTGAGAGATGAGCAAAATACATTGACCTCTATACAG 316
QY 89 TCCCTCAACTCCAGTGCACACTGAAAGCTCTGAAAGCACTGAAATATACACAGCA 148
DB 315 TCCCTGAACTTCCAGCAGACAGCTGAAGCT-TGAAGACATTAAATATATACCAATG 257
QY 149 GTAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 208
DB 256 GTGAGGATATATCTATGACCCCAAGTCATTAACCAAGTCATGATGATGATGATG 198
QY 209 TCATCATCAAGCTTAAAGAGAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 268
DB 197 TCGTGTCACCTGAGAGAGAGAGCTTGTCTGATTCCTCA--GAGTTACATACATT 140
QY 269 TTAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
DB 139 TTAATGACCTGAA-GTATGATGATGATGATGATGATGATGATGATGATGATGAT 81
QY 329 TATTTATATCATTAATCTTCCAGCAGCTATGATATATATATATATATATATAT 387
DB 80 TCTTTT-----ACTTCAGCCAGTATATGACATTAAGAAACATATTTCAAAATAC 29
QY 388 AATAAGTTAATCTATTTT 404
DB 28 AATAATGATTAATCTCTTT 12

RESULT 5

CN153669 683 bp mRNA linear EST 02-APR-2004
LOCUS DEFINITION 940808 MARC 4P1G Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CN153669
VERSION CN153669.1 GI:46168099
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 683)
AUTHORS Smith,T.P.L., Preking,B.A., Ford,J.J., Valliet,J.L., Wise,T.A.,
Noneman,D.J., Wray,J.R. and Keefe,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366

PUBMED REFERENCE AUTHORS	10349636	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komu, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE		Normalization and subtraction of cap-triapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL PUBMED AUTHORS	Genome Res. 10 (10), 1617-1630 (2000) 11042159	
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komu, H., Akiyama, T., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Katsuhagi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE		RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL PUBMED	Genome Res. 10 (11), 1757-1771 (2000) 11076861	
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE		Functional annotation of a full-length mouse cDNA collection
JOURNAL REFERENCE AUTHORS	Nature 409, 685-690 (2001) 5	
TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL REFERENCE AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 1761)	
TITLE		Adachi, S., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haru, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imocant, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komu, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE		Direct Submission
JOURNAL	Submitted (16-JUN-2001)	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES		Please visit our web site for further details.
source	URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers	1. 1761 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:A530083H05" /db_xref="taxon:10090" /clone="A530083H05" /sex="male" /tissue_type="aorta and vein" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 215. .1294
CDS		

ORIGIN	Query Match	23.6%; Score 105.6; DB 4; Length 1761;
	Best Local Similarity 58.1%; Pred. No. 4.8e-15;	
	Matches 257; Conservative 0; Mismatches 159; Indels 26; Gaps 3;	
QY	13 AGAATAATGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATTAAAGCTTCCACA 72	
Db	1303 AGAAATATGTCATTATATTCATGGAATGAAGATGAAGCAAAACATTAAATGTCAGTCACA 1362	
QY	73 CTGACCTCTTAAACAGTCCTTCAAACCTTCCAGTGCACACCTGAAGCTCTGAAGACACTG 132	
Db	1363 ATGACCTCTTGACTCAGTCATTTGTATCTCTCATGCAAGTGTGATGCTCTCAAGACCTGT 1422	
QY	133 AAATATACACACAGCAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATG 192	
Db	1423 AAACACACATTAATTAATCTGCAAGATATTTCTTCACTACCCCAAGATCATTATGAGAGCAT 1482	
QY	193 GGGCTGGGACGCTACTCATCAACCTT-----AAAAGCAGAGCTTGTCTCTC 246	
Db	1483 GTGTGTCGCGAGTTGACATTCATCAAAACATGACATGAAGAAAGACAGCTTTTCTTTTAT 1542	
QY	247 TCTTAATATGATTAACCTTCACTTAAATGACCTGTAATGTTAGATGATTAATGATGCGC 306	
Db	1543 TCTCCAAAGGATTATATCATGTTCTGATTCCTTAAAGTTAAATAT-----CC 1591	
QY	307 TACAAAAGGTAAACCTTTTATATTTTATATCAATTACTCAGGCAGCTATGATATATA 366	
Db	1592 ATTCAAGATGAGAGAGGTTTAAATAATATTTAAATCACTTTTGCACTTTTGACATCAG 1651	
QY	367 TAAACATTTTTCACACATTAATTAATGTTATCTATTTTATTTTCTAAATGTCATGTTCT 426	
Db	1652 TGAATATTT-----TCACAAAATGCACTTATTTTATTTCTTAAGTAAAGTATGCTT 1702	
QY	427 TTCCTGCTTATGATAAAGCTT 448	
Db	1703 TTTTCTTCTTGATGATGAGCTT 1724	
RESULT 10		
LOCUS	AK089895	2396 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:830047J12 product:chemokine (C-C) receptor 3, full insert sequence.	
ACCESSION	AK089895	
VERSION	AK089895.1	GI:26354724
KEYWORDS	HTC; CAP trapper.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)	
PUBMED	10349636	
REFERENCE	2	

AUTHORS	Garcinici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Komono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL PUBMED REFERENCE	Genome Res. 10 (10), 1617-1630 (2000) 11042159
AUTHORS	3 Shibata, K., Itch, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Garcinici, P., Komono, H., Akiyama, Y., Nishi, K., Kitsuana, T., Teshiro, H., Itch, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawaj, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
JOURNAL PUBMED REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 11076861
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL PUBMED REFERENCE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2396)
AUTHORS	Adechi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Garcinici, P., Fukuda, S., Furum, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizomoto, K., Higoka, T., Hirozane, T., Horii, P., Imocani, K., Ishii, Y., Itch, M., Kagawa, I., Karukawa, T., Katoh, H., Kawasaki, J., Kojima, Y., Kondo, S., Komono, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Salto, R., Salto, R., Sakai, C., Sakai, K., Sakazune, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takehashi, F., Takaku-Akihira, S., Takenaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL PUBMED REFERENCE	Direct Submission Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@res.riken.jp, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.
FEATURES	Location/Qualifiers
SOURCE	1. 2396 /organism="Mus musculus" /mol_type="mRNA" /strain="NOD" /db_xref="PANTOM DB:F830047J12" /db_xref="taxon:10090" /clone="F830047J12" /tissue_type="activated spleen" /clone_lib="RIKEN full-length enriched mouse cDNA library" 86. .1165

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			/db_xref="gi:26354725"
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ORIGIN			
Query Match	23.6%; Score 105.6; DB 4; Length 2396;		
Best Local Similarity	58.1%; Pred. No. 5e-15;		
Matches 257;	Conservative 0; Mismatches 159; Indels 26; Gaps 3;		
Db			
Qy	13 AGAAATTGCCTTAAAGAAGAACCAAGAGATGAAGCAAACACTTAAGCTTCACA 72		
1174 AGAAATTGCCTTATTCATGGA CTGAAGATGAAGCAACACTTAAGTCAGTACA 1233			
Db			
Qy	73 CTCACCTCTAAGACAGCTCTTCAAACCTTCCAGTGCCA CACTGAAGCTCTGAAGACATG 132		
1234 ATGACCTCTGCTCAGTCAGCATTTGTATCTCTCAGGCAATGGCTGATCTCAAAAACCTGT 1293			
Db			
Qy	133 AAATATACACACAGCAGTAGCACAGTAGAGATGATACCCTTAAGCTTATTAACA CAGGCCAG 192		
1294 AATACACATATATATCTCGAGATATCTTCACTTCA CCCAGATCATTAAGTAGAGACAT 1353			
Db			
Qy	193 GGCGTGGGCAAGCTACTCATCATCAACCT-----AAAAAGCAGAGCTTGTCTCTC 246		
Db	1354 GTGCTGGCCAGTTGAGCAATTCATCAACATGACATGAAAAAGACAGCTTTTTTTTTTAT 1413		
Db			
Qy	247 TCTAATAATGATTAACCTTCACTTATTAATGACCTGAATGTTAGATGTTACTATATGCCG 306		
1414 TCTCCAAAGGATTATACATGCTTCGATTCACCTTAAGGTTAAAT-----CC 1462			
Db			
Qy	307 TACAAAAGGTAAACCTTTATATTATTTATACATTA CTTACGACAGCTATGATATAA 366		
Db	1463 ATTCAACAGTAGAAGGTTTAAATAATATTAACTATCTTTGCACTTTTATGATCAG 1522		
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Qy	367 TAAAAACATTTTCAACACATTAAGTAACTATTTATTTCTAATGTCCTAGTTCT 426		
Db	1523 TGAATATTT-----TCACAAAAGCATTTATTTATTTCTTAACGTAAAGATTTCT 1573		
Db			
Qy	427 TTCCCTGCTTAATGAAAAGCTT 448		
1574 TTTTCTTCTTGATGAAATGGCTT 1595			
RESULT 11			
AK089875	2284 bp	mRNA	linear HTC 03-APR-2004
LOCUS	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F83003S018 product: chemokine (C-C) receptor 3, full insert sequence.		
ACCESSION	AK089875.1	GI:26354710	
VERSION	AK089875.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Carninci, P. and Hayashizaki, Y.		
AUTHORS	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE	2		

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159

REFERENCE AUTHORS 3

TITLE Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

REFERENCE AUTHORS 4

TITLE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

JOURNAL Functional annotation of a full-length mouse cDNA collection

REFERENCE AUTHORS Nature 409, 685-690 (2001)

TITLE 5

JOURNAL The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

REFERENCE AUTHORS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE 6 (bases 1 to 2284)

JOURNAL Adachi, J., Aizawa, K., Akimura, T., Arahawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashizaki, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Kasukawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takebe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-32 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://genome.gsc.riken.jp/. Location/Qualifiers

FEATURES

SOURCE 1. 2284

organism="Mus musculus"

molecule="mRNA"

strain="FANTOM DB:FB30035018"

db_xref="taxon:10090"

clone="FB30035018"

tissue_type="activated spleen"

clone_lib="RIKEN full-length enriched mouse cDNA library"

215. 1294

CDS

/note="unnamed protein product; chemokine (C-C) receptor 3 (MGI:104616, GB|NM_009914, evidence: BLASTN, 99%, match=1080)

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2265. 2270

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2284

/note="putative"

polyA_signal

polyA_site

2284

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ORIGIN

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73 CTCACCTCTAAAGAGAGACCAAGAGATGAGACCAACATTAAAGCTTCACCA 131

1363 ATGACCTCTTAAGAGAGACCAAGAGATGAGACCAACATTAAAGCTTCACCA 1422

132 GAATATTAACACAGACAGATGAGAGATGAGACCAACATTAAAGCTTCACCA 191

1423 TAAACACATTAATTAATGAGAGATGAGACCAACATTAAAGCTTCACCA 1482

132 GGGGCTGGGCGACGATCATTCAACCTT-----AAAAGAGAGCTTGGCTCT 245

1483 TGTGCTGGCGAGTGAACATTAATTAATTAATTAATTAATTAATTAATTAAT 1542

246 CTCCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 305

1543 TTCTCCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1591

306 CTCCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 365

1592 CATTCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1651

366 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 425

1652 GTGAATATTT-----TACCAAAATGCAATTTATTTATTTCTTAACGTAATGATTC 1702

426 TTTCCCTGCTTAATGAAGCTT 448

1703 TTTTCTTCTTGAATGAAGCTT 1725

RESULT 12

LOCUS BB223728 655 bp mRNA linear B27 31-AUG-2001

DEFINITION BB223728 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530083H05 3', mRNA sequence.

ACCESSION BB223728

VERSION BB223728.2 GI:15410154

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 655)

Arahawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,

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Query Match	16.7%; Score 75; DB 6; Length 632;	
Best Local Similarity	76.1%; Pred. No. 1.3e-07;	
Matches 118; Conservative	0; Mismatches 35; Indels 2; Gaps 2;	
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Db	480 AATTGACCTCTAATCGAGCTTTGAACCTTCACAGACGACTAAGCTC-TGAAGCA	538
Oy	130 CTGAATAATACACACAGCATGACGATGATGCATGTAACCTTAAGTCAATTAACACAGGC	189
Db	539 TTAATAATATATACACAAATGGTAGAGTATATCTATGACACCACATGATCAATCAAGAAGT	598
Oy	190 CAGGGCTGGGACAGCTACTCATCTAACCTTA 224	
Db	599 CAATGCTGGGAGTGG-ACGTGGTCAACCTGA 632	
RESULT 14		
COS683220/c	657 bp mRNA linear EST 26-JUL-2004	
LOCUS	DG11-166f13 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.	
DEFINITION	C0683220	
ACCESSION	C0683220.1 GI:50631886	
VERSION	EST.	
KEYWORDS	Canis familiaris (dog)	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ORGANISM	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;	
	Canis.	
REFERENCE	1 (bases 1 to 657)	
AUTHORS	Schlueter,T., Hermanns,J., Weindel,M., Schuetze,D., Kranz,H.,	
TITLE	Herrich,J. and Loebbert,R.	
JOURNAL	Dog arrayTAG cDNA clone collection	
COMMENT	Unpublished (2004)	
	Contact: Thomas Schlueter	
	Lion Bioscience AG	
	Weinhoferstrasse 98, D-69123 Heidelberg, Germany	
	Tel.: +49 6221 4038 150	
	Fax: +49 6221 4038 290	
	Email: Thomas.Schlueter@lionbioscience.com.	
FEATURES	Location/Qualifiers	
SOURCE	1..657	
	/organism="Canis familiaris"	
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	/strain="Beagle"	
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Best Local Similarity	66.9%; Pred. No. 1.3e-06;	
Matches 101; Conservative	0; Mismatches 50; Indels 0; Gaps 0;	
Oy	1 TAGGTCAAGTCAAGAAAATTGGCTTAAGAGGAGCACCAAGAGATGAAGCAACACTT	60
Db	154 TAAAGAGATGTGGAATTCACCTTAAGAGAGATGCACAGAACCCATGAAGCAAACATTTT	95
Oy	61 AAGCTTCACACCTCACTTAACACAGTCTTCAACTTCAGGTGACCACTGAAGCTC	120

Db	94	AAGTAATCATGTTGACCTCAAGCGCAACCCTTAAACTTCAGCTCAATGCTGTAAACCC	35
Oy	121	TTGAAGACACGAAATATATACACAGAGAATA	151
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RESULT_15			
LOCUS	CN155784	832 bp	mRNA linear EST 02-APR-2004
DEFINITION	943112 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.		
ACCESSION	CN155784		
VERSION	CN155784.1	GI:46170214	
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;		
REFERENCE	1 (bases 1 to 832) Smith,T.P.L., Preking,B.A., Ford,J.J., Vallet,J.T., Wise,T.A., Noneman,D.U., Wray,J.E. and Keesel,J.W. Porcine EST collection using a normalized library constructed from embryos representing early developmental stages Unpublished (2003) Contact: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425 c and trimmed with the aid of the trim_al option. Vector identified with cross_match v0.990329. Plate: TMW8048 row: L column: 9 Seq primer: GTAATACGACTCACTAAGGG. Location/Qualifiers 1..832 /organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 4P1G" /note="Vector: pCDNA3.1, Site_1: EcoRI, Site_2: NotI; library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."		
FEATURES			
SOURCE			
ORIGIN			
Query Match	15.0%; Score 67; DB 7; Length 832;		
Best local Similarity	67.9%; Pred. No. 1.2e-05;		
Matches	108; Conservative 0; Mismatches 50; Indels 1; Gaps 1;		
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Oy	675 AGGTCAAGTGACGAACATGTCTGAAGAAGATGAAGCAAATATATGACTCTATACAG 734		
Oy	89 TCCTTCAAACTTCCAGATGCACACTGGAAGCTCTTGAAGACCTGAAAATATACACAGCA 148		
Db	735 TCCCTTGAACCTTCAGACACGACACTGAAGCTC-TGAACACATTAATAATATATACCAATG 793		
Oy	149 GTAGACATGATGCAATGATCACTTAAGCTCANTTACACAG 187		
Db	794 GTGAGAGTATATCTATGCAACCCCAAAGTCAATTACCAAG 832		
Search completed:	January 7, 2006, 19:14:11		
Job time :	1637.64 secs		

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 03:54:36 ; Search time 244.515 Seconds
(without alignments)
12211.020 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448

Sequence: 1 tagctgcagatgcagaagaatt.....ccctgcattatgaaagctt 448

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: geneeqn1990s:*
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- 12: geneeqn2004as:*
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- 14: geneeqn2005s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	448	100.0	1717	6	AAD25221 Human che
2	448	100.0	1717	6	AAD25221 Human che
3	448	100.0	1717	6	ABE67066 Thyroid C
4	448	100.0	1717	11	AD131633 Human CDN
5	448	100.0	1717	13	AD883700 Human lym
6	448	100.0	1915	2	AAT85162 Human che
7	448	100.0	1915	10	ADC03342 Human GDN
8	448	100.0	1915	13	ADT90848 Human che
9	448	100.0	1915	13	ADU47727 Human che
10	448	100.0	5099	2	AAT93601 Human eos
11	448	100.0	5791	8	ABZ68879 Nucleotid
12	448	100.0	5791	14	ADY86631 Human CC
13	380.4	84.9	1689	2	AAT13334 CC-chemok
14	380.4	84.9	1689	2	AAT58783 Human C-C
15	380.4	84.9	1689	3	AAV07402 Human C-C
16	380.4	84.9	1689	3	AAZ55146 Human ade
17	380.4	84.9	1689	3	AAZ51268 Human low
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20	380.4	84.9	1689	10	ABX13645 Human CDN
21	380.4	84.9	1689	11	ABD20811 Human pul
22	380.4	84.9	3958	3	AAZ55147 Human ade
23	380.4	84.9	3958	3	AAZ51269 Human low
24	380.4	84.9	3958	10	ABZ96963 Human nuc
25	380.4	84.9	3958	11	ABD20812 Human pul
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27	294.4	65.7	7201	6	AB132336 Human imm
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29	108	24.1	42587	12	ADJ61642 Human oli
30	105	23.4	1201	3	AAZ55145 Human ade
31	105	23.4	1201	3	AAZ51267 Human low
32	105	23.4	1201	6	ABR4282 Human CDN
33	105	23.4	1201	8	ABZ42635 Human C-C
34	105	23.4	1201	10	ABZ96961 Human nuc
35	105	23.4	1201	10	ACA56487 Human sig
36	105	23.4	1201	11	AD131579 Human CDN
37	105	23.4	1201	11	ABD20810 Human pul
38	105	23.4	1201	12	AD156283 Human pul
39	105	23.4	1201	12	ADJ59499 Human C-C
40	105	23.4	1201	12	AD044989 Human oli
41	105	23.4	1201	13	AD883646 Human lym
42	105	23.4	1201	14	ADY15933 Human lym
43	105	23.4	1201	14	ADY15933 DNA encod
44	50	11.2	50	6	ABZ02209 Human lev
45	46.8	10.4	7025	6	ABR40060 Human che

ALIGNMENTS

RESULT 1	AAD25221	strand: DNA, 1717 BP.
ID	AAD25221	
AC	AAD25221	
XX	12-MAR-2002	(first entry)
DT	Human chemokine (C-C motif) receptor 3 (CCR3) gene #1.	
DB	Human, chemokine (C-C motif) receptor 3, CCR3 gene, haplotyping;	
XX	genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;	
KW	human immunodeficiency virus 1; single nucleotide polymorphism; SNP;	
KW	chromosome 3p21.3; ds.	
XX	Homo sapiens.	
OS		
XX		
FH	Key	Location/Qualifiers
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FT	variation	replace(197, A)
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FT	variation	205..1272
FT	variation	/*tag= c
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FT	variation	/note= "This region corresponds to exon 1"
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FT	variation	replace(1256, C)
FT	variation	/*tag= e
FT	variation	/standard name= "Single nucleotide polymorphism (SNP)"
XX	WO200187908-A2.	
XX	22-NOV-2001.	
PD	18-MAY-2001; 2001WO-US016278.	
XX	18-MAY-2001; 2000US-0205191P.	
XX	18-MAY-2000; 2000US-0205191P.	

XX (GENA-) GENA15581/07.
 PA Choi JY, Kazemi A, Koshy B;
 PI WPI, 2002-055681/07.
 XX P-PSDB; AAI51320.
 DR
 XX Isolated polymorphic variants of chemokine (C-C motif) receptor 3 (CCR3)
 PT gene useful for studying function of CCR3, expressing the CCR3 protein
 XX and to screen drugs to treat CCR3 activity-related diseases.
 XX
 PS Example 1, Fig 1, 53pp; English.
 XX
 XX The invention relates to genetic variants of human chemokine (C-C motif)
 CC receptor 3 (CCR3) gene. The invention also relates to compositions and
 CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
 CC Polynucleotides of the invention are useful for studying the expression
 CC and function of CCR3 and in expressing CCR3 proteins for use in screening
 CC candidate drugs to treat diseases related to CCR3 activity. They are also
 CC used in gene therapy. The polymorphism and haplotype data is useful for
 CC validating whether CCR3 is a suitable target for drugs to treat type IV
 CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1.
 CC screening for such drugs and reducing bias cells in clinical trials of
 CC such drugs. The genotyping method is useful for determining whether an
 CC individual has one haplotype or haplotype pairs. The haplotyping method
 CC is useful for improving the efficiency and outcome of several steps in
 CC the discovery and development of drugs for treating diseases associated
 CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
 CC The present sequence is human CCR3 gene located on chromosome 3p21.3
 CC
 SQ Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 448; DB 6; Length 1717;
 Best Local Similarity 100.0%; Pred. No. 1.4e-104;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 1 TAGGTGAGTGAAGAAATTTGCTTAAAGAGAGACCAAGAGATGAAGCAACATTT 60
 DB 1270 TAGGTGAGTGAAGAAATTTGCTTAAAGAGAGACCAAGAGATGAAGCAACATTT 1329
 XX
 61 AAGCTTCCACACTCCTCTTAAAGAGATGCTTAAAGCTTCCAGTGCACATCTGAAGCTC 120
 DB 1330 AAGCTTCCACACTCCTCTTAAAGAGATGCTTAAAGCTTCCAGTGCACATCTGAAGCTC 1389
 XX
 121 TTGAAGACCTGAAGAAATTTGCTTAAAGAGAGACCAAGAGATGAAGCAACATTT 180
 DB 1390 TTGAAGACCTGAAGAAATTTGCTTAAAGAGAGACCAAGAGATGAAGCAACATTT 1449
 XX
 181 ACCACAGGCGCAGGCGCTGGGCAAGCTGATCATCATCAACCTTAAAGAGAGCTTGGCT 240
 DB 1450 ACCACAGGCGCAGGCGCTGGGCAAGCTGATCATCATCAACCTTAAAGAGAGCTTGGCT 1509
 XX
 241 TCTCTCTTAAAGTGAATTAACCTTAAAGAGAGATGCTTAAAGTGAATTAACCTTAA 300
 DB 1510 TCTCTCTTAAAGTGAATTAACCTTAAAGAGAGATGCTTAAAGTGAATTAACCTTAA 1569
 XX
 301 TGGCGTGAAGAAAGTGAATTAACCTTAAAGAGAGATGCTTAAAGTGAATTAACCTTAA 360
 DB 1570 TGGCGTGAAGAAAGTGAATTAACCTTAAAGAGAGATGCTTAAAGTGAATTAACCTTAA 1629
 XX
 361 TATTAATTAAGAACTTTTCAACAAATTAAGTGAATTAACCTTAAAGTGAATTAACCTTAA 420
 DB 1630 TATTAATTAAGAACTTTTCAACAAATTAAGTGAATTAACCTTAAAGTGAATTAACCTTAA 1689
 XX
 421 AGTTCTTCTCTGCTTAAAGTGAATTAACCTTAAAGTGAATTAACCTTAAAGTGAATTAACCTTAA 448
 DB 1690 AGTTCTTCTCTGCTTAAAGTGAATTAACCTTAAAGTGAATTAACCTTAAAGTGAATTAACCTTAA 1717
 XX

XX
 AC AAD25245;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human chemokine (C-C motif) receptor 3 (CCR3) gene #2.
 KW Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
 KW genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
 KW human immunodeficiency virus 1; polymorphism; chromosome 3p21.3; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH
 FT misc_feature 92
 FT /tag= a
 FT /note= "This degenerate base represents polymorphic site (PS) 1"
 FT (PS) 1
 FT misc_feature 197
 FT /tag= b
 FT /note= "This degenerate base represents polymorphic site (PS) 2"
 FT (PS) 2
 FT misc_feature 255
 FT /tag= c
 FT /note= "This degenerate base represents polymorphic site (PS) 3"
 FT (PS) 3
 FT misc_feature 1256
 FT /tag= d
 FT /note= "This degenerate base represents polymorphic site (PS) 4"
 FT (PS) 4
 XX
 PN WO200187908-A2.
 XX
 PD 22-NOV-2001.
 XX
 PP 18-MAY-2001; 2001WO-US016278.
 XX
 PR 18-MAY-2000; 2000US-0205191P.
 XX
 PA (GENA-) GENA15581/07.
 XX
 PI Choi JY, Kazemi A, Koshy B;
 XX
 DR WPI, 2002-055681/07.
 XX
 PT Isolated polymorphic variants of chemokine (C-C motif) receptor 3 (CCR3)
 PT gene useful for studying function of CCR3, expressing the CCR3 protein
 XX and to screen drugs to treat CCR3 activity-related diseases.
 XX
 PS Claim 5, Page 53; 53pp; English.
 XX
 XX The invention relates to genetic variants of human chemokine (C-C motif)
 CC receptor 3 (CCR3) gene. The invention also relates to compositions and
 CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
 CC Polynucleotides of the invention are useful for studying the expression
 CC and function of CCR3 and in expressing CCR3 proteins for use in screening
 CC candidate drugs to treat diseases related to CCR3 activity. They are also
 CC used in gene therapy. The polymorphism and haplotype data is useful for
 CC validating whether CCR3 is a suitable target for drugs to treat type IV
 CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1.
 CC screening for such drugs and reducing bias cells in clinical trials of
 CC such drugs. The genotyping method is useful for determining whether an
 CC individual has one haplotype or haplotype pairs. The haplotyping method
 CC is useful for improving the efficiency and outcome of several steps in
 CC the discovery and development of drugs for treating diseases associated
 CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
 CC The present sequence is human CCR3 gene located on chromosome 3p21.3
 CC
 SQ Sequence 1717 BP; 434 A; 427 C; 350 G; 502 T; 0 U; 4 Other;
 XX
 Query Match 100.0%; Score 448; DB 6; Length 1717;
 Best Local Similarity 100.0%; Pred. No. 1.4e-104;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	TAGGTGCAATGCAGAAAATTGGCTTAAAGAGAAAGGACCAAGAGATGAAGCAACACTT	60
Db	1270	TAGGTGCAATGCAGAAAATTGGCTTAAAGAGAAAGGACCAAGAGATGAAGCAACACTT	1329
OY	61	AAGCTTTCACACTCACCCTCTTAAACAGTCTCTTCAACCTTCAGTGCACACTGAAGTTC	120
Db	1330	AAGCTTTCACACTCACCCTCTTAAACAGTCTCTTCAACCTTCAGTGCACACTGAAGTTC	1389
OY	121	TTGAAAGACACTGAAATATATACACAGCAGTGAAGCTATATGCATGTAACCTTAAGTCAAT	180
Db	1390	TTGAAAGACACTGAAATATATACACAGCAGTGAAGCTATATGCATGTAACCTTAAGTCAAT	1449
OY	181	ACCAAGGCGCAGGGGCTGGGAGGCTACTCATCATCAACCTTAAAAAGCAGAGCTTGGCT	240
Db	1450	ACCAAGGCGCAGGGGCTGGGAGGCTACTCATCATCAACCTTAAAAAGCAGAGCTTGGCT	1509
OY	241	TCTCTCTCTTAAATGAGTTTACCTTACATTTTATATGCACTGAATGTTAGATGTTACTATAT	300
Db	1510	TCTCTCTCTTAAATGAGTTTACCTTACATTTTATATGCACTGAATGTTAGATGTTACTATAT	1569
OY	301	TGCGGCTCAAAAAGGTAAACCTTTTATATTTTATATCAATTAACCTTCAGCAGCTATATGA	360
Db	1570	TGCGGCTCAAAAAGGTAAACCTTTTATATTTTATATTAATTAATTAACCTTCAGCAGCTATATGA	1629
OY	361	TATATAATAAACATTTTCACACAAATACATAAAGTTAACTATTTTATTTTCTAAATGTGCTT	420
Db	1630	TATATAATAAACATTTTCACACAAATACATAAAGTTAACTATTTTATTTTCTAAATGTGCTT	1689
OY	421	AGTCTTTTCCCTGCTTATTAAGAAAGCTT 448	
Db	1690	AGTCTTTTCCCTGCTTATTAAGAAAGCTT 1717	

RESULT 3	
ABL67066	
ID	ABL67066 standard; DNA, 1717 BP.
XX	
AC	ABL67066;
XX	
DT	15-MAY-2002 (first entry)
XX	
DE	Thyroid cancer related gene sequence SEQ ID NO:5403.
XX	
KW	Human; cancer; colon; prostate; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US010838.
XX	
PR	05--JUN-2000; 2000US-0209473P.
PR	05--JUN-2000; 2000US-0209531P.
PR	18-SEP-2000; 2000US-0231133P.
PR	18-SEP-2000; 2000US-0233617P.
PR	20-SEP-2000; 2000US-0234009P.
PR	20-SEP-2000; 2000US-0234034P.
PR	20-SEP-2000; 2000US-0234052P.
PR	22-SEP-2000; 2000US-0234509P.
PR	22-SEP-2000; 2000US-0234567P.
PR	25-SEP-2000; 2000US-0234924P.
PR	25-SEP-2000; 2000US-0234924P.
PR	25-SEP-2000; 2000US-0235077P.
PR	25-SEP-2000; 2000US-0235082P.
PR	25-SEP-2000; 2000US-0235134P.
PR	25-SEP-2000; 2000US-0235280P.
PR	26-SEP-2000; 2000US-0235637P.

PR	26-SEP-2000	2000US-0235638P.
PR	27-SEP-2000	2000US-0235711P.
PR	27-SEP-2000	2000US-0235729P.
PR	27-SEP-2000	2000US-0235840P.
PR	27-SEP-2000	2000US-0235863P.
PR	28-SEP-2000	2000US-0236028P.
PR	28-SEP-2000	2000US-0236032P.
PR	28-SEP-2000	2000US-0236033P.
PR	28-SEP-2000	2000US-0236034P.
PR	28-SEP-2000	2000US-0236109P.
PR	28-SEP-2000	2000US-0236111P.
PR	29-SEP-2000	2000US-0236842P.
PR	29-SEP-2000	2000US-0236891P.
PR	02-OCT-2000	2000US-0237172P.
PR	02-OCT-2000	2000US-0237173P.
PR	02-OCT-2000	2000US-0237279P.
PR	02-OCT-2000	2000US-0237294P.
PR	02-OCT-2000	2000US-0237295P.
PR	02-OCT-2000	2000US-0237316P.
PR	03-OCT-2000	2000US-0237425P.
PR	03-OCT-2000	2000US-0237595P.
PR	03-OCT-2000	2000US-0237604P.
PR	03-OCT-2000	2000US-0237606P.
PR	03-OCT-2000	2000US-0237608P.
PR	01-NOV-2000	2000US-0244867P.
PR	01-NOV-2000	2000US-0245084P.

Young PB, Augustus M, Carter KC, Edner R, Endress G, Horrigan S, Soppet DR, Weaver Z; MPI, 2002-188264/24.

WPI; 2002-188264/24

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 5403; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, (1) has cytostatic activity and can be used in gene therapy, M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, cervical, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell, carcinoma, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms's tumour.

Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;

Query Match 100.0%; Score 440; DB 6; Length 1717;

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      GC Content    = 20.86% ;
      Matches       = 448; Conservative   0; Mismatches     0; Indels        0; Gaps          0;

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Db 1270 TAGGTGAGATGCAGAAAATTGCTTAAAGAGAGACCAAGAGATGAAGCAAAACATT 1320

61 AAGCTTCACACTCCTCTAAACAGTCTTCAACTTCACAGTCACACCTGAAGCTC 120

121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGATGATACCTAAGTCA TT 180

DB 1390 TTGAAGACACTGAAATATACACACAGAGTAGAGATGACATGACCTTAAGTCATT 1449
 QY 181 ACCACAGGCGAGGGGCTGGGACAGCTATCATCATCAACCCCTTAAGAGAGCTTGGCT 240
 DB 1450 ACCACAGGCGAGGGGCTGGGACAGCTATCATCATCAACCCCTTAAGAGAGAGCTTGGCT 1509
 QY 241 TCTCTCTCTAAATGAGTACCTACATTTTAATGACCTGAATGTTAGTACTATTA 300
 DB 1510 TCTCTCTCTAAATGAGTACCTACATTTTAATGACCTGAATGTTAGTACTATTA 1569
 QY 301 TGGCGGTACAAAAGGTAAAGCTTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAA 360
 DB 1570 TGGCGGTACAAAAGGTAAAGCTTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAA 1629
 QY 361 TATTAATATAAATCTTTTACACATATCAATTAAGTAACTTAACTTAACTTAACTTAACTTAA 420
 DB 1630 TATTAATATAAATCTTTTACACATATCAATTAAGTAACTTAACTTAACTTAACTTAACTTAA 1689
 QY 421 AGTTCCTTCCCTGCTTAATGAAAAGCTT 448
 DB 1690 AGTTCCTTCCCTGCTTAATGAAAAGCTT 1717

RESULT 4
 ADI31633
 ID ADI31633 standard; cDNA; 1717 BP.

AC ADI31633;
 DT 17-JUN-2004 (first entry)
 DE Human cDNA #959.

Human; gene; ss; immunological response; immunopathological condition;
 Crohn's disease; asthma; ulcerative colitis; hypersensitivity;
 Irritable Bowel Syndrome; osteoarthritis; rheumatoid arthritis;
 acute monocytic leukemia; anti-inflammatory; antiaesthetic; antitumor;
 osteoporosis; antiarthritic; antirheumatic; cytostatic.

OS Homo sapiens.
 XX US6607879-B1.
 XX 19-AUG-2003.
 XX 09-FEB-1998; 98US-00023655.
 XX 09-FEB-1998; 98US-00023655.
 XX (INCY-) INCYTE CORP.
 XX Cocks BG, Stuart SG, Selhamer JJ;
 DR WPI; 2003-895307/82.

A composition comprising a plurality of cDNAs, useful for detecting
 altered expression of genes in an immunological response or for
 diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
 or osteoarthritis.

claim 1, SEQ ID NO 959; 50bp; English.

The invention relates to a composition comprising a plurality of cDNAs
 for detecting the altered expression of genes in an immunological
 response. The invention also relates to a method of diagnosing or
 monitoring the treatment of an immunopathological condition in a sample,
 comprising obtaining nucleic acids from a sample, contacting the nucleic
 acids of the sample with an array comprising the plurality of cDNAs under
 conditions to form one or more hybridisation complexes, detecting the
 hybridisation complexes and comparing the levels of the detected
 hybridisation complexes with the level of hybridisation complexes
 detected in a non-diseased sample, where an altered level of the detected

CC hybridisation complexes correlates with the presence of an
 CC immunopathological condition. Also disclosed are an expression profile
 CC comprising a microarray and a plurality of detectable complexes and a
 CC method for identifying a plurality of polynucleotide probes. The cDNAs
 CC are useful as hybridisable array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray can be used in
 CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
 CC ulcerative colitis, hypersensitivity, irritable bowel syndrome,
 CC osteoarthritis, rheumatoid arthritis or acute monocytic leukemia, and in
 CC identifying agents for the treatment of the diseases. The microarray may
 CC also be used in drug discovery and development, toxicological and
 CC carcinogenicity studies, forensic or pharmacogenomics. The composition
 CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
 CC genomic fragments. This sequence represents a human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 11; Length 1717;

Best Local Similarity 100.0%; Pred. No. 1.4e-104;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAATGACGAGAAATGCTTAAAGAGAGACCAAGAGATGAGACAAACATT 60
 DB 1270 TAGGTCAATGACGAGAAATGCTTAAAGAGAGACCAAGAGATGAGACAAACATT 1329
 QY 61 AAGCTTCCACACTACCTCTTAAACAGCTTTTAAAGCTTCAAGTCAACCTGAAGCTC 120
 DB 1330 AAGCTTCCACACTACCTCTTAAACAGCTTTTAAAGCTTCAAGTCAACCTGAAGCTC 1389
 QY 121 TTGAAGACACTGAAATATACACACAGAGTAGAGATGACATGACCTTAAGTCATT 180
 DB 1390 TTGAAGACACTGAAATATACACACAGAGTAGAGATGACATGACCTTAAGTCATT 1449
 QY 181 ACCACAGGCGAGGGGCTGGGACAGCTATCATCATCAACCCCTTAAGAGAGCTTGGCT 240
 DB 1450 ACCACAGGCGAGGGGCTGGGACAGCTATCATCATCAACCCCTTAAGAGAGAGCTTGGCT 1509
 QY 241 TCTCTCTCTAAATGAGTACCTACATTTTAATGACCTGAATGTTAGTACTATTA 300
 DB 1510 TCTCTCTCTAAATGAGTACCTACATTTTAATGACCTGAATGTTAGTACTATTA 1569
 QY 301 TGGCGGTACAAAAGGTAAAGCTTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAA 360
 DB 1570 TGGCGGTACAAAAGGTAAAGCTTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAA 1629
 QY 361 TATTAATATAAATCTTTTACACATATCAATTAAGTAACTTAACTTAACTTAACTTAACTTAA 420
 DB 1630 TATTAATATAAATCTTTTACACATATCAATTAAGTAACTTAACTTAACTTAACTTAACTTAA 1689
 QY 421 AGTTCCTTCCCTGCTTAATGAAAAGCTT 448
 DB 1690 AGTTCCTTCCCTGCTTAATGAAAAGCTT 1717

RESULT 5
 ADS83700
 ID ADS83700 standard; cDNA; 1717 BP.

ADS83700;
 DT 11-AUG-2005 (first entry)

Human lymph node cDNA #959.

ss; gene; human; immunological response; blood cell; cancer;
 immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
 bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
 osteoporosis; pancreatitis; infection; arthritis; lymph node.
 OS Homo sapiens.

XX US2004077003-A1.
XX
XX 22-APR-2004.
XX
XX 14-AUG-2003; 2003US-00641643.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Selthamer JJ;
XX
XX WPI; 2004-387937/36.
XX
XX
XX New compositions having a number of first, second and third
XX polynucleotide probes, useful in research and diagnostic applications in
XX cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
XX infections.
XX
XX Claim 15; SEQ ID NO 959; 16pp; English.
XX
XX The invention relates to polynucleotides which are used as probes to
XX detect genes differentially expressed in an immunological response,
XX abundantly expressed in an immunological response and/or coding for a
XX polypeptide known to regulate blood cell biology. The polynucleotides are
XX useful in research and diagnostic applications particularly in cancer and
XX immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
XX atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
XX sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
XX present sequence represents a human lymph node cDNA used to detect blood
XX cell and immunological response gene expression. Note: The present
XX sequence does not appear in the printed specification but was obtained in
XX electronic format from the USPTO web site
XX (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
XX Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 448; DB 13; Length 1717;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-104;
XX Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TAGGTGAGTGCAGAAATATGCTTAAGAGAGAGAGAGAGATGAAGCAACATT 60
XX |||||
XX 1270 TAGGTGAGTGCAGAAATATGCTTAAGAGAGAGAGAGAGATGAAGCAACATT 1329
XX
XX 61 AAGCCTTCACACTCACTCTTAAGAGAGAGAGAGAGATGAAGCAACATT 120
XX |||||
XX 1330 AAGCCTTCACACTCACTCTTAAGAGAGAGAGAGAGATGAAGCAACATT 1389
XX
XX 121 TTGAAGACACTGAAATATATACACAGAGAGAGAGAGAGATGAAGCAACATT 180
XX |||||
XX 1390 TTGAAGACACTGAAATATATACACAGAGAGAGAGAGAGATGAAGCAACATT 1449
XX
XX 181 ACCACAGGCGAGGCGGTGGGAGAGAGAGAGAGAGATGAAGCAACATT 240
XX |||||
XX 1450 ACCACAGGCGAGGCGGTGGGAGAGAGAGAGAGAGATGAAGCAACATT 1509
XX
XX 241 TCTCTCTCTAAATAGTACCTACATTTTAATGACCTGAATGTTAGTAGTACTATA 300
XX |||||
XX 1510 TCTCTCTCTAAATAGTACCTACATTTTAATGACCTGAATGTTAGTAGTACTATA 1569.
XX
XX 301 TGGCGGTACAAAGGTAAAGCTTTTAAATTTTAACTTAACCTTACAGCGATTTGA 360
XX |||||
XX 1570 TGGCGGTACAAAGGTAAAGCTTTTAAATTTTAACTTAACCTTACAGCGATTTGA 1629
XX
XX 361 TTTAAATTAAGCTTTTACACATATCAATTAAGTAACTTTTAACTTAAGTAACTT 420
XX |||||
XX 1630 TTTAAATTAAGCTTTTACACATATCAATTAAGTAACTTTTAACTTAAGTAACTT 1689
XX
XX 421 AGTTCTTTCCCTGCTTAATGAAGGCTT 448
XX |||||
XX 1690 AGTTCTTTCCCTGCTTAATGAAGGCTT 1717
XX
XX

RESULT 6
AAT85162
ID AAT85162 standard; cDNA; 1915 BP.
XX
XX AAT85162;
XX
XX 14-DEC-1997 (first entry)
XX
XX
XX Human chemokine receptor 88-2B cDNA.
XX
XX Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; human; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT CDS 362..1429
XX FT /*tag= a
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX P-PSDB; AAW27124.
XX
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX
XX Claim 7; Page 48-50; 65pp; English.
XX
XX
XX This sequence comprises a full-length cDNA coding for novel human
XX chemokine receptor 88-2B (AAW27124), a G protein coupled receptor that is
XX involved in leukocyte trafficking. The 88-2B cDNA was obtained from a
XX macrophage cDNA library using 88-2B-specific primers. A full-length clone
XX (see AAT89161) for chemokine receptor 88C (AAW27123) was also obtained.
XX 88C and 88-2B cDNAs can be used to produce recombinant polypeptides in
XX transformed host cells for use in the treatment of e.g. atherosclerosis,
XX rheumatoid arthritis, tumours, asthma, viral infection, AIDS and
XX inflammatory conditions. Nucleic acid fragments can be used to isolate
XX genomic sequences, to detect alleles of the gene (for diagnosis or in
XX gene therapy), to alter receptor genetics to facilitate identification of
XX modulators and to produce knockout animals, and (antisense forms) to
XX alter/study the genetics and expression of the receptor
XX
XX
XX Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 448; DB 2; Length 1915;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-104;
XX Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX |||||
XX 1487 AAGCCTTCACACTCACTCTTAAGAGAGAGAGAGAGATGAAGCAACATT 1546
XX
XX 121 TTGAAGACACTGAAATATATACACAGAGAGAGAGAGAGATGAAGCAACATT 180
XX |||||
XX

XX	KW	infection; vaccine; virucide; gene; ss.
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FT	CDS	/tag= c
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FT	misc_feature	/tag= b
FT	FT	/note= "Encodes extracellular domain"
FT	FT	539..574
FT	FT	/tag= d
FT	FT	/note= "Encodes extracellular domain"
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FT	FT	/note= "Encodes extracellular domain"
FT	FT	1016..1081
FT	FT	/tag= h
FT	FT	/note= "Encodes extracellular domain"
FT	FT	1148..1213
FT	FT	/tag= i
FT	FT	/note= "Encodes intracellular domain"
FT	FT	1277..1426
FT	FT	/tag= j
FT	FT	/note= "Encodes intracellular domain"
FT	FT	1430..1915
FT	FT	/tag= k
XX	PV	US6797811-B1.
XX	PD	28-SEP-2004.
XX	PP	20-DEC-1996; 96US-00771276.
XX	PR	20-DEC-1995; 95US-00575967.
XX	PR	07-JUN-1996; 96US-00661393.
XX	PA	(ICOS-) ICOS CORP.
XX	P1	Gray PM, Schweickart VL, Raport CJ;
XX	DR	WPI, 2004-687775/67.
XX	DR	P-PESDB; ADR90849.
XX	PT	New antibodies specifically binding to (the extracellular domain of) a
XX	PT	chemokine receptor 88C polypeptide expressed on the surface of cells,
XX	PT	useful for inhibiting human or simian human immunodeficiency infection of
XX	PT	such cells.
PS	Example 2, SEQ ID NO 3; 2pp; English.	
CC	XX	The invention relates to a novel antibody that specifically binds to the
CC	XX	extracellular domain of a chemokine receptor 88C or 88-2B polypeptide
CC	XX	expressed on the surface of cells. The antibody fails to cross-react with
CC	XX	an MCP-1 receptor (CCR2) and is useful for inhibiting human or simian
CC	XX	immunodeficiency virus (HIV or SIV) infection of the cells expressing
CC	XX	chemokine receptor 88C or 88-2B. The invention is also used to detect 88C
CC	XX	or 88-2B gene products their analogues or biologically active fragments.
CC	XX	The antibody products may be used to as modulators of receptor activities
CC	XX	or to diagnose tissue-specific variations in expression of 88-2B or 88C.
CC	XX	The invention is also used in the preparation of vaccines. The present
CC	XX	sequence is the human chemokine receptor 88-2B CDNA.
SEQ	XX	Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

	Query Match	Score 448; DB 13; Length 1915;	
	Best Local Similarity	100.0%; Pred. No. 1,5e-104;	
	Matches 448; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Oy	1 TAGGTCAAGATGCAGAAAATTGCTTAAAGAAGAACCAAGAGATGAAGCAAACACTT	60	
Dd	1427 TAGGTCAAGATGCAGAAAATTGCTTAAAGAAGAACCAAGAGATGAAGCAAACACTT	1480	
Oy	61 AAGCCTTCACACTCACCTCTTAAACAGTCCCTTGAAACTTCAGTGCACAACCTGAAGCTC	120	
Dd	1487 AAGCCTTCACACTCACCTCTTAAACAGTCCCTTGAAACTTCAGTGCACAACCTGAAGCTC	1544	
Oy	121 TTGAAGACACTGAAATATPACACAGCAGTAGAGCATGATGATACCTTAAGGTCAAT	180	
Dd	1547 TTGAAGACACTGAAATATPACACAGCAGTAGAGCATGATGATACCTTAAGGTCAAT	1600	
Oy	181 ACCAAGGCCAGGGGCGTGGGAGCGGTACTCATCATCAACCCTAAAAAGCAGCTTTGCT	240	
Dd	1607 ACCAAGGCCAGGGGCGTGGGAGCGGTACTCATCATCAACCCTAAAAAGCAGCTTTGCT	166	
Oy	241 TCTCTCTTAAAGAAGTACTCTACATTTTATGCACTGAAATGTAATAGTACTATA	300	
Dd	1667 TCTCTCTTAAAGAAGTACTCTACATTTTATGCACTGAAATGTAATAGTACTATA	172	
Oy	301 TGCGGCTACAAAAAGGTAAACCTTTTTATTTTATTAATTAACCTTCAGCCAGTATTA	360	
Dd	1727 TGCGGCTACAAAAAGGTAAACCTTTTTATTTTATTAATTAACCTTCAGCCAGTATTA	178	
Dd	361 TATTAATTAACATTTTCACACAATATCAATTAAGTTAACTATTTTATTTCTATATGCTT	420	
Oy	1787 TATTAATTAACATTTTCACACAATATCAATTAAGTTAACTATTTTATTTCTATATGCTT	184	
Oy	421 AGTCTTTCCCTGCTATATGAAGAAGCTT 448		
Dd	1847 AGTCTTTCCCTGCTATATGAAGAAGCTT 1874		
RESULT 9			
ADU47727 standard; cDNA, 1915 BP.			
ID	ADU47727	standard; cDNA, 1915 BP.	
AC	ADU47727;		
XX			
DT	10-FEB-2005	(first entry)	
XX			
DS	Human chemokine receptor 88-2B cDNA.		
KX	Chemokine receptor; 88c; human immunodeficiency virus;		
KX	simian immunodeficiency virus; HIV; SIV; MCP-1; CCKR-2; 88-2B;		
KW	leukocyte trafficking; acquired immune deficiency syndrome; AIDS;		
KW	psoriasis; rheumatoid arthritis; atherosclerosis; tumor; asthma;		
KM	viral infection; inflammation; anti-HIV; virucide; antiproliferic;		
OS	antiarthritic; antiarteriosclerotic; antiinflammatory; human; gene; 88.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	5'UTR	1..361	
FT		/*tag= a	
FT	CDS	362..1429	
FT		/*tag= b	
FT		/product= "Chemokine receptor 88-2B "	
FT	3'UTR	1430..1915	
FT		/*tag= c	
XX			
PN	US2004230037-A1.		
XX			
PD	18-NOV-2004.		
XX			
PF	04-FEB-2004; 2004US-00772037.		
XX			
PR	20-DEC-1995; 95US-00575967.		

```
PR 07-JUN-1996; 96US-00661393.
PR 20-DEC-1996; 96US-00771276.
PA (ICOS-) ICOS CORP.
PI Gray PM, Schweickart VL, Raport CJ;
XX WPI; 2004-813308/80.
XX P-PSDB; AD047728.
XX
XX Modulating chemokine receptor 88C-mediated human or simian
XX immunodeficiency virus infection comprises administering an antibody that
XX binds to chemokines or a polypeptide comprising an antigen-binding
XX fragment of the antibody.
XX
XX Example 2; SEQ ID NO 3; 28pp; English.
XX
XX The invention relates to a method of modulating chemokine receptor 88C-
XX mediated human or simian immunodeficiency virus (HIV or SIV) infection of
XX cells. The method comprises administering to a mammalian subject a
XX composition comprising an antibody or a polypeptide comprising an antigen
XX -binding fragment of the antibody, where the mammalian subject is
XX infected with HIV or SIV, and where the antibody is administered in an
XX amount that modulates HIV or SIV infection of 88C-expressing cells in the
XX subject. The antibody is a humanised antibody which specifically binds to
XX the extracellular domain of the chemokine receptor 88C polypeptide and
XX fails to cross-react with an MCP-1 receptor (CCR-2) or binds to the N-
XX terminal 20 amino acid peptide of the 88C receptor. The invention also
XX provides purified and isolated nucleic acids encoding chemokine
XX receptors, namely 88-2B and 88-C, involved in leukocyte trafficking. The
XX modulators of the chemokine receptors of the invention are useful for
XX treating diseases such as HIV or SIV infection (e.g. acquired immune
XX deficiency syndrome (AIDS)), psoriasis, rheumatoid arthritis,
XX atherosclerosis, tumour growth suppression, asthma, viral infection, or
XX inflammation. The present sequence is the human chemokine receptor 88-2B
XX cDNA.
XX
XX Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 448; DB 13; Length 1915;
Best Local Similarity 100.0%; Pred. No. 1.5e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGTGAGTGCAGAAAATTGCTTAAGAGAGAGACCAAGAGATGAAGCAACATT 60
DB 1427 TAGTTCAGATGCAGAAAATTGCTTAAGAGAGAGACCAAGAGATGAAGCAACATT 1486
QY 61 AAGCCTTCACACTCCTCTTAAGAGAGAGACCAAGAGATGAAGCAACATT 120
DB 1487 AAGCCTTCACACTCCTCTTAAGAGAGAGACCAAGAGATGAAGCAACATT 1546
QY 121 TTGAAGACACTGAATATATACACACAGAGATGAGATGATGACCTTAAGTCAATT 180
DB 1547 TTGAAGACACTGAATATATACACACAGAGATGAGATGATGACCTTAAGTCAATT 1606
QY 181 ACCACAGGCGAGGGGCTGGGCGAGCTGATCATCATCAACCTTAAGAGAGAGCTTGT 240
DB 1607 ACCACAGGCGAGGGGCTGGGCGAGCTGATCATCATCAACCTTAAGAGAGAGCTTGT 1666
QY 241 TCTCTCTTAAGATGATTAACCTTAAGAGAGAGCTTGT 300
DB 1667 TCTCTCTTAAGATGATTAACCTTAAGAGAGAGCTTGT 1726
QY 301 TGCAGCTACAAAAGGTTAAATCTTTATATATATATATATATATATATATATATAT 360
DB 1727 TGCAGCTACAAAAGGTTAAATCTTTATATATATATATATATATATATATATATAT 1786
QY 361 TATATAATAAACAATTTTCAACAATAACAATAAGTAACTATATATATATATATATAT 420
DB 1787 TATATAATAAACAATTTTCAACAATAACAATAAGTAACTATATATATATATATATAT 1846
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
```

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DB 1847 AGTTCTTCCCTGCTTAATGAAAAGCTT 1874
RESULT 10
AAT93601
ID AAT93601 standard; cDNA; 5099 BP.
XX
XX AAT93601;
XX
XX 07-MAY-1998 (first entry)
XX
XX Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
XX
XX Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;
XX atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
XX beta-chemokine receptor; viral infection; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX misc_feature 1..3586
XX /tag= a
XX /note= "5' genomic DNA flanking sequence"
XX CDS 3587..4654
XX /tag= b
XX /product= "human eosinophil eotaxin receptor"
XX misc_feature 4655..5099
XX /tag= c
XX /note= "terminator region"
XX
XX W09741154-A1.
XX
XX 06-NOV-1997.
XX
XX 24-APR-1997; 97WO-US006568.
XX
XX 26-APR-1996; 96US-0016158P.
XX 26-APR-1996; 96US-0017113P.
XX 17-JAN-1997; 97GB-00000894.
XX
XX (MERL ) MERCK & CO INC.
XX
XX Daugherty BL, Demartino JA, Springer MS, Siciliano SJ;
XX
XX WPI; 1997-549685/50.
XX P-PSDB; AAW31850.
XX
XX New isolated human eosinophil eotaxin receptor - used to develop products
XX for treating and preventing atopic conditions e.g. allergic rhinitis,
XX dermatitis, conjunctivitis and bronchial asthma.
XX
XX Claim 12, 13, 14; Page 16-20; 51pp; English.
XX
XX This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
XX pair sequence comprises a 1065 base pair open reading frame encoding a
XX 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'
XX genomic DNA sequence and a 3' terminator region. This novel eosinophil
XX eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
XX Agents which bind to this eosinophil eotaxin receptor can be used for the
XX treatment and prevention of atopic conditions such as allergic rhinitis,
XX dermatitis, conjunctivitis and bronchial asthma. Agents which block this
XX eosinophil eotaxin receptor can be used to prevent viral infection in
XX healthy individuals and slow or halt viral progression in infected
XX patients
XX
XX Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 448; DB 2; Length 5099;
Best Local Similarity 100.0%; Pred. No. 1.9e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGTGAGTGCAGAAAATTGCTTAAGAGAGAGACCAAGAGATGAAGCAACATT 60
```

DB 4652 TAGGTCAAGTCAGAGAAATTGCTTAAGAGAGACCAAGAGATGAACAAACATT 4711
QY 61 AAGCCTTCACACTCACTCAAAACAGTCCTTAACCTTCAAGTCACACTGAAGCTC 120
DB 4712 AAGCCTTCACACTCACTCAAAACAGTCCTTCAAACTTCAAGTCACACTGAAGCTC 4771
QY 121 TTGAAGACACTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 180
DB 4772 TTGAAGACACTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 4831
QY 181 ACCACAGGCGAGGCGTGGGCGAGCTACTCATCATCAACCTTAAGAGAGAGCTTGGCT 240
DB 4832 ACCACAGGCGAGGCGTGGGCGAGCTACTCATCATCAACCTTAAGAGAGAGCTTGGCT 4891
QY 241 TCTCTCTCAAAATAGATTAACCTTAATGACCTGAAGTGAATGATTAATTA 300
DB 4892 TCTCTCTCAAAATAGATTAACCTTAATGACCTGAAGTGAATGATTAATTA 4951
QY 301 TCCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATATAT 360
DB 4952 TCCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATAT 5011
QY 361 TATTAATATAAATTTTCAACATATCAATTAATTAATTTTATATATATATATATATAT 420
DB 5012 TATTAATATAAATTTTCAACATATCAATTAATTAATTTTATATATATATATATATAT 5071
QY 421 AGTTCTTTCCCTGCTTAATGAAGCTT 448
DB 5072 AGTTCTTTCCCTGCTTAATGAAGCTT 5099

RESULT 11

ABZ68879 standard; cDNA; 5791 BP.

XX AC ABZ68879;
XX DT 28-MAY-2003 (first entry)
XX DE Nucleotide sequence of human chemokine receptor CCR3.
XX KW Human; chemokine receptor; CCR3; viral infection; surface protein;
XX KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma; gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 4015..5082
XX FT /tag= a
XX FT /product= "CCR3"
XX PN WO2003014153-A2.
XX PD 20-FEB-2003.
XX PF 12-AUG-2002; 2002WO-CA001248.
XX PR 10-AUG-2001; 2001US-0311088P.
XX PA (TOP1-) TOPIGEN PHARM INC.
XX PI Renzi P, Zemzouni K;
XX DR WPI; 2003-256541/25.
XX DR P-PSDB; ABP97726.
XX PT Modulating viral infection of a cell, for treating or preventing
XX PT respiratory virus infections, bronchitis, pneumonia or asthma, by
XX PT modulating a binding interaction between a cell chemokine-receptor and a
XX PT surface protein of the virus.
XX PS Disclosure; Page 84-88; 120pp; English.

XX CC The present sequence encodes human chemokine receptor CCR3. The
CC specification describes a method for modulating viral infection of a
CC cell. The method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX SQ Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 8; Length 5791;

Best Local Similarity 100.0%; Pred. No. 2e-104;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTCAGAGAAATTGCTTAAGAGAGACCAAGAGATGAACAAACATT 60
DB 5080 TAGGTCAAGTCAGAGAAATTGCTTAAGAGAGACCAAGAGATGAACAAACATT 5139
QY 61 AAGCCTTCACACTCACTCAAAACAGTCCTTCAAACTTCAAGTCACACTGAAGCTC 120
DB 5140 AAGCCTTCACACTCACTCAAAACAGTCCTTCAAACTTCAAGTCACACTGAAGCTC 5199
QY 121 TTGAAGACACTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 180
DB 5200 TTGAAGACACTGAATATATACACAGCAGTAGAGATGATGATGATGATGATGATGAT 5259
QY 181 ACCACAGGCGAGGCGTGGGCGAGCTACTCATCATCAACCTTAAGAGAGAGCTTGGCT 240
DB 5260 ACCACAGGCGAGGCGTGGGCGAGCTACTCATCATCAACCTTAAGAGAGAGCTTGGCT 5319
QY 241 TCTCTCTCAAAATAGATTAACCTTAATGACCTGAAGTGAATGATTAATTA 300
DB 5320 TCTCTCTCAAAATAGATTAACCTTAATGACCTGAAGTGAATGATTAATTA 5379
QY 301 TCCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATATAT 360
DB 5380 TCCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATAT 5439
QY 361 TATTAATATAAATTTTCAACATATCAATTAATTAATTTTATATATATATATATATAT 420
DB 5440 TATTAATATAAATTTTCAACATATCAATTAATTAATTTTATATATATATATATATAT 5499
QY 421 AGTTCTTTCCCTGCTTAATGAAGCTT 448
DB 5500 AGTTCTTTCCCTGCTTAATGAAGCTT 5527

RESULT 12

ADY86631 standard; DNA; 5791 BP.

XX AC ADY86631;
XX DT 02-JUN-2005 (first entry)
XX DE Human CC chemokine receptor 3 (CCR3) gene.
XX KW Gene expression; screening; multiple sclerosis; neuroprotective;
XX KW immune disorder; neurological disease; DNA microarray; gene; ds;
XX KW chemokine.
XX OS Homo sapiens.
XX PN US2005064483-A1.
XX PD 24-MAR-2005.
XX PF 30-AUG-2004; 2004US-00929182.
XX PR 28-AUG-2003; 2003US-0498731P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Zang JZ, Hong J;
 XX WPI, 2005-252668/26.
 XX GENBANK; AF247361.
 XX
 XX Monitoring multiple sclerosis patient taking beta-interferon or
 XX glatiramer acetate to predict treatment response by determining
 XX expression profile of inflammatory nucleic acids using RNA of patient and
 XX comparing to control.
 XX
 XX Claim 1; SEQ ID NO 21; 73bp; English.
 XX
 XX The present invention relates to gene expression profiling technology to
 XX quantitatively measure the expression profiles of genes selected based on
 XX their role in inflammation and their susceptibility to regulation by
 XX current multiple sclerosis (MS) treatment agents by isolating RNA from
 XX peripheral blood mononuclear cells (PBMC) of patient. The invention is
 XX particularly useful for monitoring a multiple sclerosis patient taking
 XX interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
 XX treatment response. The present sequence is human CC chemokine receptor 3
 XX (CCR3) gene. This gene is used to illustrate the evaluation of PBMC
 XX responses to in vitro treatment with IFN-beta or GA agents by gene
 XX expression profiling technology.
 XX
 XX Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 14; Length 5791;
 Best Local Similarity 100.0%; Pred. No. 2e-104;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTGAGTGGAGAAATTTGCTTAAGAAGAGAGACAGAGAGATGAAGAAACATT 60
 DB TAGGTGAGTGGAGAAATTTGCTTAAGAAGAGAGACAGAGAGATGAAGAAACATT 5139
 QY 61 AAGCCTTCACACTCACTCTTAAGACATCTTCAAACTTCCAGTGCACACTGAAGCTC 120
 DB AAGCCTTCACACTCACTCTTAAGACATCTTCAAACTTCCAGTGCACACTGAAGCTC 5199
 QY 121 TTGAAGACACTGAATATATACACAGACAGATGAGATGATGATGATGATGATGAT 180
 DB TTGAAGACACTGAATATATACACAGACAGATGAGATGATGATGATGATGATGAT 5259
 QY 181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCCCTAAAAGCAGACTTGGCT 240
 DB ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCCCTAAAAGCAGACTTGGCT 5319
 QY 241 TCTCTCTTAATATGATTAACCTTAATGAATGATGATGATGATGATGATGATGAT 300
 DB TCTCTCTTAATATGATTAACCTTAATGAATGATGATGATGATGATGATGATGAT 5379
 QY 301 TGGCGCTACAAAAGTAAAGCTTTTATATTTTATATATATATATATATATATATAT 360
 DB TGGCGCTACAAAAGTAAAGCTTTTATATTTTATATATATATATATATATATATAT 5439
 QY 361 TTTAATTAATAAATTTCACACATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 DB TTTAATTAATAAATTTCACACATTAATTAATTAATTAATTAATTAATTAATTAATTA 5499
 QY 421 AGTTCTTTCCTGCTTAATGAAGCTT 448
 DB AGTTCTTTCCTGCTTAATGAAGCTT 5527

RESULT 13
 AAT31334
 ID AAT31334 standard; DNA; 1689 BP.
 XX AAT31334;
 AC
 XX 15-NOV-1996 (first entry)
 DT

XX CC-chemokine receptor 3 genomic DNA.
 XX
 XX CC-chemokine receptor 3; CRP-3; Bos-l2; inhibitor; antisense;
 XX antiinflammatory; eosinophil; ds.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FH CDS 181..1248
 XX FT /tag= a
 XX FT 1007..1008
 XX FT variation
 XX FT /tag= b
 XX FT /note= "CCR-3 genomic clone has CG at positions 1007-
 XX 1008, coding for threonine (ACG) at position 276; a cDNA
 XX clone has GC at these positions, coding for serine (AGC)"
 XX FT misc_difference 1291
 XX FT /tag= c
 XX FT /note= "base n at position 1291 is not identified in the
 XX specification"

XX W09622371-A2.
 XX 25-JUL-1996.
 XX 19-JAN-1996; 96WO-US000608.
 XX 19-JAN-1995; 95US-00375199.
 XX
 XX (LEUK-) LEUKOSITE INC.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;
 XX WPI; 1996-354528/35.
 XX P-PSDB; AAW03376.

XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
 XX identify receptor inhibitors to treat inflammatory disease, e.g.
 XX autoimmune disorders, certain cancers, etc.
 XX
 XX Claim 1; Page 109; 153bp; English.

XX A genomic DNA clone (T31334) codes for a novel receptor (W03376),
 XX designated Bos l2 or C-C chemokine receptor 3 (CCR-3), involved in
 XX leukocyte migration associated with inflammation. It was isolated from a
 XX human genomic library from eosinophil cDNA using degenerate primers (see
 XX also T31337-44). A CCR-3 cDNA clone (T31335) was also isolated, and a
 XX consensus sequence is given in T31336. The genomic and cDNA clones can be
 XX used for the prodn. of recombinant CCR-3 in host cells, or to design
 XX antisense sequences useful for treating inflammatory disease

XX Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 0 U; 1 Other;
 Query Match 84.9%; Score 380.4; DB 2; Length 1689;
 Best Local Similarity 98.4%; Pred. No. 2.9e-87;
 Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY 7 AGATGCAAAAATTTGCTTAAGAAGAGACCAAGAGATGAAGCAACACTTAAGCTT 66
 DB AGATGCAAAAATTTGCTTAAGAAGAGACCAAGAGATGAAGCAACACTTAAGCTT 1310
 QY 67 TCCACACTCACTCTTAAGACATCTTCAAACTTCCAGTGCACACTGAAGCTTGA 125
 DB TCCACACTCACTCTTAAGACATCTTCAAACTTCCAGTGCACACTGAAGCTTGA 1369
 QY 126 GACACTGAATATTAACACAGCAGATGAGATGATGATGATGATGATGATGATGAT 185
 DB GACACTGAATATTAACACAGCAGATGAGATGATGATGATGATGATGATGATGAT 1429
 QY 186 AGGCCAGGGGGCTGGGAGCGTACTCATCATCAACCCCTAAAAGCAGAGCTTGTCTCT 245

CC	AAV07402	standard; DNA; 1689 BP.
XX	AAV07402;	
AC	AAV07402;	
XX	28-SEP-1998	(first entry)
DT	28-SEP-1998	(first entry)
XX		
DE	Human C-C chemokine receptor 3 genomic DNA.	
XX		
KM	C-C chemokine receptor 3; CCR3; Eos I2; human;	
KM	G protein-coupled receptor; leukocyte; antibody; antagonistic;	
KM	inflammation; allergy; asthma; graft rejection; infection;	
KM	autoimmune disease; drug screening; therapy; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	181..1248
FT		/*tag= a
XX		
PN	W09814480-A1.	
XX		
PD	09-APR-1998.	
XX		
XX	24-SEP-1997;	97MO-US017103.
PR	30-SEP-1996;	96US-00720565.
XX		
PA	(LEUK-) LEUKOSITE INC.	
XX		
PI	Mackay CR, Ponath PD;	
DR	WPI: 1998-286418/25.	
XX	P-PeDB; AAW51744.	
PT	Antibodies to chemokine receptor-3 protein - useful for diagnosis and	
PT	treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune	
PT	disease, graft rejection or cancer.	
XX		
PS	Example 2; Fig 1A-C; 185bp; English.	
XX		
CC	This genomic DNA codes for novel human C-C chemokine receptor 3 (see	
CC	AAW51744), also designated CCR-3, CCR3 or Eos I2, that binds and mediates	
CC	chemotaxis in response to chemokines such as eotaxin, RANTES and MCP-3.	
CC	The DNA was isolated from a human genomic phase library using as probe a	
CC	PCR fragment that had been generated from eosinophil cDNA using primers	
CC	(see AAV07405-12) based on known chemokine receptor genes. A cDNA clone	
CC	(see AAV07403) for CCR-3 is also provided. Comparison of the sequences	
CC	suggests that the genomic DNA has an intron that separates the promoter	
CC	and most of the 5' untranslated region from the coding region. A	
CC	consensus of the genomic and cDNA sequences is provided (see AAV07404).	
CC	The invention relates to isolated and/or recombinant nucleic acids	
CC	encoding CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant	
CC	nucleic acid constructs, host cells useful for production of recombinant	
CC	CCR-3 proteins, to antibodies reactive with the receptors, and to methods	
CC	of using these products to identify ligands, antagonists and agonists of	
CC	receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory	
CC	or allergic diseases and conditions, including respiratory allergic	
CC	diseases such as asthma, allergic rhinitis, hypersensitivity lung	
CC	disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.	
CC	Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung	
CC	disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with	
CC		

CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing
CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses,
CC drug allergy, insect sting allergy, inflammatory bowel disease, such as
CC Crohn's disease and ulcerative colitis, spondyloarthropathy, scleroderma,
CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
CC myositis and eosinophilic fasciitis; autoimmune diseases such as
CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
CC rejection, including allograft rejection or graft-versus-host disease;
CC cancers with leukocyte infiltration of the skin or organs; and also
CC reperfusion injury, atherosclerosis, certain hematologic malignancies,
CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used
CC for treating: immunosuppression e.g. in AIDS patients or individuals
CC undergoing radiation therapy, chemotherapy, therapy for autoimmune
CC disease or other drug therapy, and immunosuppression due congenital
CC deficiency in receptor function or other causes; and infectious diseases
CC such as parasitic diseases, including helminth infections, such as
CC nematodes (round worms). The agents can also be used for detection and
CC diagnosis

XX
SQ Sequence 1689 BP, 431 A; 416 C; 344 G; 497 T; 0 U; 1 Other;

Query Match 84.9%; Score 380.4; DB 2; Length 1689;
Best Local Similarity 98.4%; Pred. No. 2.9e-87;
Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5

QY	7	AGATGCGAAATTTGGCCCTAAAGAGAAAGACCTCAAGAGATGAAACAACATTAAAGCT	66
Db	1251	AGATGCGAAATTTGGCTTAAGAGAGAGACCTCAAGATTAAGCAACATTAAAGCT	13110
QY	67	TCCACTCATCCTCTAAACAGTCCCTCAAA - CTCGAGTGCACACTGAAGCTCTTGA	125
Db	1311	TCCACTCATCCTCTAAACAGTCCCTCAAACTTCGAGTGCACACTGAAGCTCTT - AA	13683
QY	126	GACACTGAAATATATACACAGCAGTATGAGATGATGATGATACCTTAAGGTCATTACAC	185
Db	1370	GACACTGAAATATATACACAGCAGTATGAGATGATGATGATACCTTAAGGTCATTACAC	14228
QY	186	AGGCGAGGGGCTGGGCGAGCTACTCATCATCAACCTTAAAAAGCAGAGCTTGGCTTCT	245
Db	1430	AGGCGCA - GGGCTGGGCGAGCTACTCATCATCA - CTTAAAAAGCAGAGCTTGGCTTCT	1487
QY	246	CTCTAAATGAGTTACTTACATTTTAAATGACCTGAAAGTTAGATGTTACTTAATATGCG	305
Db	1488	CTCTAAATGAGTTACTTATTTTAAATGACCTGAAAGTTAGATGTTACTTAATATGCG	1547
QY	306	CTACAAAAGGTTAAACTTTTATATTATTAATACATTAACTTCAGCGACCTATTGATATTA	365
Db	1548	CTACAAAAGGTTAAACTTTTATATTATTAATACATTAACTTCAGCGACCTATT - ATATTA	1600
QY	366	ATTAACAATTTTCAACACATACAAATTAAGTTAACTATTTTATTTTCTAATGTCCTAGTTC	425
Db	1607	ATTAACAATTTTCAACACATACAAATTAAGTTAACTATTTTATTTCTAATGTCCTAGTTC	1666
QY	426	TTTCCCTGCTTAATGAAAAGCTT 448	
Db	1667	TTTCCCTGCTTAATGAAAAGCTT 1689	

Search completed: January 7, 2006, 07:04:58
Job time : 246.515 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:41:27 ; Search time 2207.58 seconds
(without alignment)
11535.651 Million cell updates/sec

Title: US-10-767-521-4
Perfect score: 448
Sequence: 1 tagctcagatcgacgaagaatt.....ccctcctatcgaaagcct 448

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_in: 3: gb_env: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pr: 9: gb_ro: 10: gb_scs: 11: gb_by: 12: gb_un: 13: gb_vl: 14: gb_hcg: 15: gb_pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	448	6	AR164121
2	448	100.0	448	6	BD128571
3	448	100.0	448	6	AX030931
4	448	100.0	1717	6	AR380414
5	448	100.0	1717	6	AX334894
6	448	100.0	1717	6	HSU51241
7	448	100.0	1915	6	ARS84940
8	448	100.0	1915	6	BD006761
9	448	100.0	1915	6	BD017703
10	448	100.0	5791	6	AX705064
11	448	100.0	5791	6	AF247361
12	448	100.0	177334	8	AC138069
13	448	100.0	177334	8	AC138069
14	448	100.0	220865	14	HSN312688
15	385	85.9	1913	8	AK123050
16	380.4	84.9	1689	6	BD082060
17	380.4	84.9	1689	6	AR300121
18	380.4	84.9	1689	6	AR475065

19	380.4	84.9	1689	6	ARS91370	ARS91370 Sequence
20	380.4	84.9	1689	8	HSU49727	U49727 Human C-C c
c 21	339.2	75.7	7201	6	AX345239	AX345239 Sequence
22	294.4	65.7	7201	6	AX345238	AX345238 Sequence
c 23	178.6	39.9	144233	4	AP006435	AP006435 Sus scrofa
24	178.6	39.9	167298	4	AP006436	AP006436 Sus scrofa
c 25	155.4	34.7	1678	4	AB119270	AB119270 Sus scrofa
26	155.4	34.7	1838	4	AB119269	AB119269 Sus scrofa
c 27	118.4	26.4	816	10	BV208413	BV208413 CCR3 515
28	111.2	24.8	110000	14	AC098557_2	Continuation (3 of
29	111.2	24.8	216520	14	AC112542	AC112542 Rattus no
c 30	105.6	23.6	163404	9	AC140491	AC140491 Mus muscu
31	105	23.4	1201	6	CS032233	CS032233 Sequence
c 32	105	23.4	1201	6	CS035919	CS035919 Sequence
33	105	23.4	1201	6	CS041185	CS041185 Sequence
c 34	105	23.4	1201	6	CS044871	CS044871 Sequence
35	105	23.4	1201	6	CS129103	CS129103 Sequence
c 36	105	23.4	1201	6	AR270522	AR270522 Sequence
37	105	23.4	1201	6	AR380360	AR380360 Sequence
c 38	105	23.4	1201	6	AX548778	AX548778 Sequence
39	105	23.4	1201	6	HSU28694	U28694 Human eosin
c 40	105	23.4	1202	6	CO714581	CO714581 Sequence
41	56.2	12.5	1440	9	MMU28406	U28406 Mus musculu
c 42	50.6	11.3	164233	5	CR752649	CR752649 Zebrafish
c 43	48.4	10.8	349980	6	AX344574	AX344574 Sequence
c 44	48.2	10.8	348034	2	CR382400	CR382400 Plasmodiu
c 45	47.4	10.6	168406	14	AC090770	AC090770 Homo sapi

ALIGNMENTS

RESULT 1	AR164121	448 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	AR164121	Sequence 4 from patent US 6271347.			
DEFINITION	AR164121				
ACCESSION	AR164121				
VERSION	AR164121.1	GI:16235067			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 448)				
AUTHORS	Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.				
TITLE	Rosinophil lectarin receptor				
JOURNAL	Patent: US 6271347-A 4 07-AUG-2001;				
FEATURES	Location/Qualifiers				
source	1..448				
ORIGIN	/organism="Unknown"				
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Query Match	100.0%; Score 448; DB 6; Length 448;				
Best Local Similarity	100.0%; Pred. No. 2.7e-83;				
Matches	448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	TTGGTCAGATGCGAGAAATTCCTTAAGAGAGGACCAAGAGATGAGCAACACATT	60		
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QY	61	AAGCCTTCACACTCACTCTTAAACAGCTCTTCAAACTTCCAGTGCACACTGAGCTC	120		
DB	61	AAGCCTTCACACTCACTCTTAAACAGCTCTTCAAACTTCCAGTGCACACTGAGCTC	120		
QY	121	TTGAAGACCTGAATATACACACGAGGAGGAGTGAATGATGATGATGATGATGATGAT	180		
DB	121	TTGAAGACCTGAATATACACACGAGGAGGAGTGAATGATGATGATGATGATGATGAT	180		
QY	181	ACCAAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240		
DB	181	ACCAAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240		
QY	241	TCT	300		

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QY 361 TATAAATAAATTAATTTTACACATTAATAGTTAACTTATTTATTTCTATATGTGCT 420
Db 361 TATAAATAAATTAATTTTACACATTAATAGTTAACTTATTTATTTCTATATGTGCT 420
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
Db 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448

RESULT 2
BD128571 448 bp DNA linear PAT 18-SEP-2002
LOCUS BD128571
DEFINITION Eosinophil eotaxin receptor.
ACCESSION BD128571.1 GI:23223516
VERSION JP 2002503950-A/3.
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 448)
AUTHORS Daugherty,B.L., Demartino,J.A., Springer,M.S. and Siciliano,S.J.
TITLE Eosinophil eotaxin receptor
JOURNAL Patent: JP 2002503950-A 3 05-FEB-2002;
MERCK & CO INC

COMMENT

OS Unidentified
PN JP 2002503950-A/3
PD 05-FEB-2002
PR 24-APR-1997 JP 1997539970
PR 26-APR-1996 US 08/640991,26-APR-1996 US 60/016158 PR
17-JAN-1997 GB 9700894.0
PI BRUCE J, DAUGHERTY,JULIE A DEMARTINO,MARTIN S SPRINGER PI
,SALVATORE J SICILIANO
PC C07K14/705,C07K14/715,C12N15/12
CC Strandedness: Single;
CC Topology: Linear;
CC Eosinophil eotaxin receptor
FH Key Location/Qualifiers
FT source 1..448
Location/Qualifiers
1..448
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ORIGIN

Query Match 100.0%; Score 448; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTGAAGAAATTTGCTTAAGGAAAGACCAAGAGATGAAGCAACATT 60
Db 1 TAGGTCAAGTGAAGAAATTTGCTTAAGGAAAGACCAAGAGATGAAGCAACATT 60
QY 61 AAGCCTTCACACTCACTCTTAACAGATCCTTCAAACTTCCAGTCAACACTGAAGCTC 120
Db 61 AAGCCTTCACACTCACTCTTAACAGATCCTTCAAACTTCCAGTCAACACTGAAGCTC 120
QY 121 TTGAAGACACTGAATATATACACAGAGATGAGATGATGATGATGATGATGATGAT 180
Db 121 TTGAAGACACTGAATATATACACAGAGATGAGATGATGATGATGATGATGATGAT 180
QY 181 ACCACAGGCAAGGAGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGAGCTTGCT 240
Db 181 ACCACAGGCAAGGAGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGAGCTTGCT 240
QY 240 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
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QY 241 TCTCTCTAAAGTACCTTAAATGACCTGAATGTAGATCTATTA 300
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QY 301 TGGCGCTCAAAAAGGTAAACCTTTTATTTATTTATACATTAAGTACGAGCTATTGA 360
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Db 361 TATAAATAAATTAATTTTACACATTAATAGTTAACTTATTTATTTCTATATGTGCT 420
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
Db 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448

RESULT 3
AX030931 448 bp DNA linear PAT 20-SEP-2000
LOCUS AX030931
DEFINITION Sequence 4 from Patent EP1012190.
ACCESSION AX030931
VERSION AX030931.1 GI:10278336
KEYWORDS
SOURCE unclassified
ORGANISM unclassified sequences.

REFERENCE 1
AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLE Eosinophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 4 28-JUN-2000;
MERCK & CO INC (US)

FEATURES
source 1..448
Location/Qualifiers
1..448
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ORIGIN

Query Match 100.0%; Score 448; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAAGTGAAGAAATTTGCTTAAGGAAAGACCAAGAGATGAAGCAACATT 60
Db 1 TAGGTCAAGTGAAGAAATTTGCTTAAGGAAAGACCAAGAGATGAAGCAACATT 60
QY 61 AAGCCTTCACACTCACTCTTAACAGATCCTTCAAACTTCCAGTCAACACTGAAGCTC 120
Db 61 AAGCCTTCACACTCACTCTTAACAGATCCTTCAAACTTCCAGTCAACACTGAAGCTC 120
QY 121 TTGAAGACACTGAATATATACACAGAGATGAGATGATGATGATGATGATGATGAT 180
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QY 181 ACCACAGGCAAGGAGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGAGCTTGCT 240
Db 181 ACCACAGGCAAGGAGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGAGCTTGCT 240
QY 241 TCTCTCTAAAGTACCTTAAATGACCTGAATGTAGATCTATTA 300
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Db 361 TATAAATAAATTAATTTTACACATTAATAGTTAACTTATTTATTTCTATATGTGCT 420
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
Db 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448

TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

FEATURES
source Location/Qualifiers
1.1717
/organism="Homo sapiens"
/mol_type="genomic DNA"
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205.1272
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205.1272
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VTGILKTLRCSKKKKAIRLIFVIMAFPIIPMTPVNVAIILSSYQILPQNDERS
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ORIGIN
Query Match 100.0%; Score 448; DB 8; Length 1717;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAGATGCAAAAATTGCTTAAAGAGAGAGCAAGAGATGAACAACACTT 60
DB 1270 TAGGTCAGATGCAAAAATTGCTTAAAGAGAGAGCAAGAGATGAACAACACTT 1329
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DB 1330 AAGCTTCCACACTCAGCTCTTAAACAGTCCCTTCAACCTTCCAGTGCACACTGAAGCTC 1389
QY 121 TTGAAGACACTGAATATATACACACAGCAGTAGAGTAGAGTAGACCTTAAGGTCATT 180
DB 1390 TTGAAGACACTGAATATATACACACAGCAGTAGAGTAGAGTAGACCTTAAGGTCATT 1449
QY 181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAGAGAGCTTGGCT 240
DB 1450 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAGAGAGCTTGGCT 1509
QY 241 TCTCTCTCTAAATAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 300
DB 1510 TCTCTCTCTAAATAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1569
QY 301 TGCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATATATAT 360
DB 1570 TGCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATATAT 1629
QY 361 TATAATATAAATTTTCAACATATCAATTAAGTAACTTATTTTCTATATGTCCT 420
DB 1630 TATAATATAAATTTTCAACATATCAATTAAGTAACTTATTTTCTATATGTCCT 1689
QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
DB 1690 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1717

RESULT 7
AR584940 AR584940 1915 bp mRNA linear PAT 15-DEC-2004
LOCUS AR584940 Sequence 3 from patent US 6797811.
DEFINITION AR584940
ACCESSION AR584940
VERSION AR584940.1 GI:56627916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gray,P.W., Schweickart,V.L. and Raport,C.J.
TITLE Antibodies to chemokine receptor 88C
JOURNAL Patent: US 6797811-A 3 28-SEP-2004;
Icos Corporation; Bothell, WA

FEATURES
source Location/Qualifiers
1.1915
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ORIGIN
Query Match 100.0%; Score 448; DB 6; Length 1915;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1427 TAGGTCAGATGCAAAAATTGCTTAAAGAGAGAGCAAGAGATGAACAACACTT 1486
QY 61 AAGCTTCCACACTCAGCTCTTAAACAGTCCCTTCAACCTTCCAGTGCACACTGAAGCTC 120
DB 1487 AAGCTTCCACACTCAGCTCTTAAACAGTCCCTTCAACCTTCCAGTGCACACTGAAGCTC 1546
QY 121 TTGAAGACACTGAATATATACACACAGCAGTAGAGTAGAGTAGATGATGATGATGATGATG 180
DB 1547 TTGAAGACACTGAATATATACACACAGCAGTAGAGTAGAGTAGATGATGATGATGATGATG 1606
QY 181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAGAGAGCTTGGCT 240
DB 1607 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAGAGAGCTTGGCT 1666
QY 241 TCTCTCTCTAAATAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 300
DB 1667 TCTCTCTCTAAATAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1726
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DB 1727 TGCCGCTACAAAAGGTAAACCTTTTATATTTTATATATATATATATATATATATATATAT 1786
QY 361 TATAATATAAATTTTCAACATATCAATTAAGTAACTTATTTTCTATATGTCCT 420
DB 1787 TATAATATAAATTTTCAACATATCAATTAAGTAACTTATTTTCTATATGTCCT 1846
QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
DB 1847 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874

RESULT 8
BD006761
LOCUS BD006761 1915 bp DNA linear PAT 31-JUN-2002
DEFINITION Chemokine receptors 88-2B [CCR-3] and 88c and antibodies thereof.
ACCESSION BD006761
VERSION BD006761.1 GI:18635132
KEYWORDS JP 2001029089-A/2.
SOURCE JP 2001029089-A/2.
ORGANISM unidentified.
unclassified.
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary,P.W., Sheicart,V.L. and Raport,C.J.
TITLE Chemokine receptors 88-2B [CCR-3] and 88c and antibodies thereof
JOURNAL Patent: JP 2001029089-A 2 06-FEB-2001;
ICOS CORP
OS Unidentified
PN JP 2001029089-A/2
PD 06-FEB-2001
PF 16-MAY-2000 JP 2000143832
PR 20-DEC-1995 US 08/575967 07-JUN-1996 US 08/661393 PI
PATRICK W GARY, VICOMKI L SHEICART CARROLL J RAYPORT PC
C12N15/09, C07K14/715, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, PC

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	Query Match 100.0%; Score 448; DB 6; Length 1915; Best Local Similarity 100.0%; Pred. No. 2,1e-83; Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 TAGGTCAATGCAGAAATTTCTTAAGAAGAACCAAGAGATGAAGACAACTT 60	
Db	1427 TAGTCAGATCGAATAATTGGCTTAAGAGAGAACCAAGAGATGAAGACAACTT 1486	
Oy	61 AAGCTTCCACACTCACCTCTAACAAGTCTTCMACTTCAGTGCAACCTGAAGCTC 120	
Db	1487 AAGCTTCCACACTCACCTCTAACAAGTCTTCMACTTCAGTGCAACCTGAAGCTC 1546	
Oy	121 TTGAAGACCTGAATATATACACAGCATGTACATGATGATGATGATGATGATGAT 180	
Db	1547 TTGAAGACCTGAATATATACACAGCATGTACATGATGATGATGATGATGATGAT 1606	
Oy	181 ACCACAGGCCAGGGGCTGGGAGGATCACTCAATCAACCCTAAAAGCAGAGCTTGCT 240	
Db	1607 ACCACAGGCCAGGGGCTGGGAGGATCACTCAATCAACCCTAAAAGCAGAGCTTGCT 1666	
Oy	241 TCTCTCTTAATAAGATTACTCAATTTATATGCACTGATGATGATGATGATGATGAT 300	
Db	1667 TCTCTCTTAATAAGATTACTCAATTTATATGCACTGATGATGATGATGATGATGAT 1726	
Oy	301 TGCGGCTACAAAAAGTTAAACCTTTATATTTATATATTAATTAATTAATTAATTA 360	
Db	1727 TGCGGCTACAAAAAGTTAAACCTTTATATTTATATATTAATTAATTAATTAATTA 1786	
Oy	361 TATAATAAAACATTTTACACAAATTAACAATGAATTAATTAATTTATTAATGTCCT 420	
Db	1787 TATAATAAAACATTTTACACAAATTAACAATGAATTAATTAATTTATTAATGTCCT 1846	
Oy	421 AGTCTTTCCTCGCTTAATGAAGCTT 448	
Db	1847 AGTCTTTCCTCGCTTAATGAAGCTT 1874	
RESULT 9		
LOCUS	BD017703	1915 bp DNA linear PAT 27-AUG-2002
DEFINITION	Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof.	
ACCESSION	BD017703	
VERSION	BD017703.1 GI:2255879	
KEYWORDS	JP 2001264324-A/2.	
SOURCE	unidentified	
ORGANISM	unidentified	
REFERENCE	1 (bases 1 to 1915)	
AUTHORS	Gary, P.W., Schweickart, V.L. and Raport, C.J.	
TITLE	Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof	
JOURNAL	Patent: JP 2001264324-A 2 26-SEP-2001;	
COMMENT	OS Unidentified	
	PN JP 2001264324-A/2	
	PD 26-SEP-2001	

[illegible]

TITLE Cellular virus receptors and methods of use
JOURNAL Patent: WO 03014153-A 5-20-FEB-2003;
Topigen Pharmaceutical Inc (CA)
FEATURES Location/Qualifiers
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4015..5082
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AVLAALPERIFETBELPEPTICSAIYPEDVYSRHRHTLMTIFCVLPLVMAIC
YTGIIKTLIRCPSSKKRYKALRIIFVIMAVPFIPTVYVAILLSYQSIIRGNDERS
KHLIDVMLVTEVIASHCCMNPVIYAFVGERFRKYLRFPHRLMLHGRYIPLPSS
KLERTSSVSPSTABEPLSIV"

ORIGIN
Query Match 100.0%; Score 448; DB 6; Length 5791;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS
1 TAGGTCAAGTGCAGAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACT 60
5080 TAGGTCAAGTGCAGAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACT 5139
61 AAGCTTCACACTCACTCTTAACAGTCTTCAACTCCAGTGCAACACTGAAGCTC 120
5140 AAGCTTCACACTCACTCTTAACAGTCTTCAACTCCAGTGCAACACTGAAGCTC 5199
121 TTGAAGACACTGAATATATACACAGCAGTAGACAGATGATGATGATGATGAT 180
5200 TTGAAGACACTGAATATATACACAGCAGTAGACAGATGATGATGATGATGAT 5259
181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTGGT 240
5260 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTGGT 5319
241 TCTCTCTCTAAATGATTAAGTAAATGCACTGGAATGTTAGTAACTACTATA 300
5320 TCTCTCTCTAAATGATTAAGTAAATGCACTGGAATGTTAGTAACTACTATA 5379
301 TGGCGCTCAAAAAGGTAAAGCTTTTATATTTTATACATTAAGTCAAGCAGTATGA 360
5380 TGGCGCTCAAAAAGGTAAAGCTTTTATATTTTATACATTAAGTCAAGCAGTATGA 5439
361 TATAATATAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 420
5440 TATAATATAAATTTTCAACATATCAATTAAGTAACTATTTTCTAATGCTCT 5499
421 AGTCTTTTCCGTGCTTAATGAAGCTT 448
5500 AGTCTTTTCCGTGCTTAATGAAGCTT 5527

RESULT 11
AF247361 5791 bp DNA linear PRI 26-JUN-2002
LOCUS AF247361
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.
ACCESSION AF247361
VERSION AF247361.1 GI:19110542
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 5791)
REFERENCE
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

TITLE Michael,N.L.
JOURNAL Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
PUBMED for a Rare XRAY-Less Promoter Structure Conserved between
12079287 Drosophila and Humans
GENOMICS 80 (1), 86-95 (2002)
REFERENCE
AUTHORS 2 (bases 1 to 5791)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
JOURNAL Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA

FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="13"
/map="3p21; between CCR1 and CCR5"
/clone="11A5, frag B"
/cell_type="peripheral blood mononuclear cell"
<1..5562
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/gene="CCR3"
/product="CC chemokine receptor 3"
<4004..5562
/gene="CCR3"
/product="CC chemokine receptor 3"
4015..5082
/gene="CCR3"
/note="CCR3; G-protein coupled seven transmembrane
spanning receptor; principle cell-surface receptor for
eosinophil family of chemokines; expressed on eosinophils,
CD4/Th2 and CD8 lymphocytes, monocytes, microglia, and
dendritic cells"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAL85154.1"
/db_xref="GI:19110543"
/translation="MTSLDVTVEFGTTSYYDDVGLCEKADTRALMAQFVPLYSLV
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HGMCLLSGFYHTGYSLEPIILITIDRYLAIVHVAVALRAVTFGTISIVTMGL
AVLAALPERIFETBELPEPTICSAIYPEDVYSRHRHTLMTIFCVLPLVMAIC
YTGIIKTLIRCPSSKKRYKALRIIFVIMAVPFIPTVYVAILLSYQSIIRGNDERS
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KLERTSSVSPSTABEPLSIV"

ORIGIN
polyA_signal 5542..5547
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polyA_site 5562
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Query Match 100.0%; Score 448; DB 8; Length 5791;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS
1 TAGGTCAAGTGCAGAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACT 60
5080 TAGGTCAAGTGCAGAAATTGCTTAAGAGAGAGCAAGAGATGAAGCAACACT 5139
61 AAGCTTCACACTCACTCTTAACAGTCTTCAACTCCAGTGCAACACTGAAGCTC 120
5140 AAGCTTCACACTCACTCTTAACAGTCTTCAACTCCAGTGCAACACTGAAGCTC 5199
121 TTGAAGACACTGAATATATACACAGCAGTAGACAGATGATGATGATGATGAT 180
5200 TTGAAGACACTGAATATATACACAGCAGTAGACAGATGATGATGATGATGAT 5259
181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTGGT 240
5260 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCTTAAGAGAGCTTGGT 5319

QY 241 TCTCTCTAAATAGTACCTACATTTTAAATGACCTGAATGTTAGTACTATATA 300
| | | | |
Db 5320 TCTCTCTAAATAGTACCTACATTTTAAATGACCTGAATGTTAGTACTATATA 5379
| | | | |
QY 301 TCCCGCTCAAAAAGGTAAACCTTTTATATTTATACATTAACCTTACCCGCTATTGA 360
| | | | |
Db 5380 TCCCGCTCAAAAAGGTAAACCTTTTATATTTTATACATTAACCTTACCCGCTATTGA 5439
| | | | |
QY 361 TATAATATAAATATTTTACACATATCAATATAGTTAATTTTATTTTCTATATGAGCT 420
| | | | |
Db 5440 TATAATATAAATATTTTACACATATCAATATAGTTAATTTTATTTTCTATATGAGCT 5499
| | | | |
QY 421 AGTTCTTCTCCCTGCTTAATGAAAAGCTT 448
| | | | |
Db 5500 AGTTCTTCTCCCTGCTTAATGAAAAGCTT 5527
| | | | |
RESULT 12
AC138069 177334 bp DNA 1linear PRI 19-FEB-2003
LOCUS AC138069
DEFINITION Homo sapiens chromosome 3 clone RP13-54612, complete sequence.
ACCESSION AC138069.3 GI:28416170
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and
Haugen, B.D.
Direct Submission
Unpublished
2 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, B.D.
Direct Submission
Submitted (12-DEC-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, B.D.
Direct Submission
Submitted (10-JAN-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 177334)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and
Haugen, B.D.
Direct Submission
Submitted (19-FEB-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Feb 19, 2003 this sequence version replaced gi:27573398.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UMG
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP13-54612 (bc0820)
----- Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177210 bases at least Q40
Consensus quality: 177313 bases at least Q30
Consensus quality: 177334 bases at least Q20
Insert size: 177334, sum-of-contigs
Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-793815 (UMGC:bc0564) AC104439, 95469-bp overlap

3': U95626, 42710-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

BcoRI

BglII

SeqDerMap	FragPrint	SeqDerMap	FragPrint	SeqDerMap	FragPrint
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1239	1199	11125	10952	6306	6319
-----	-----	-----	-----	-----	-----
449	<800	2290	2310	2067	2071
-----	-----	-----	-----	-----	-----
510	<800	560	<800	3913	3756
-----	-----	-----	-----	-----	-----
6511	6363	54	<800	2169	2210
-----	-----	-----	-----	-----	-----
5296	5509	1159	1158	910	910
-----	-----	-----	-----	-----	-----
10424	10027	4052	4034	875	883
-----	-----	-----	-----	-----	-----
5046	5119	1846	1829	3716	3756
-----	-----	-----	-----	-----	-----
1196	1199	8334	8273	4502	4523
-----	-----	-----	-----	-----	-----
1397	1392	12882	12573	1967	1945
-----	-----	-----	-----	-----	-----
2597	2624	448	<800	2864	2871
-----	-----	-----	-----	-----	-----
1688	1674	12737	12573	4724	4738
-----	-----	-----	-----	-----	-----
3800	3818	10300	10103	4773	4738
-----	-----	-----	-----	-----	-----
2248	2269	6671	6656	3707	3756
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1074	1055	4052	4034	336	<800
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7303	7718	1392	1386	79	<800
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959	959	4253	4286	4736	4738
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551	<800	2791	2834	1889	1945
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1074	1055	2647	2682	3696	3756
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5688	5759	3423	3409	1569	1539
5183	5363	73	<800	8078	8038
3100	3093	499	<800	1365	1325
921	959	723	<800	289	<800
4350	4244	2763	2834	11047	10790
4331	4857	6594	6656	8848	8663
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
3900	3818	1613	1641	1787	1756
1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945
1174	1155	520	<800	1707	1631
7015	7139	219	<800	3835	3756
2852	2868	1571	1503	6586	6551
221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800	-----	-----	3255	3265
1026	1055	-----	-----	183	<800
14333	14484	-----	-----	3128	3144
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Query Match 100.0%; Score 448; DB 8; Length 177334;
Best Local Similarity 100.0%; Pred. No. 9.8e-84;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAATGACGAAATTCGCTTAAAGAGAGGACCAAGAGATGAAGCAACACTT 60
DB 89456 TAGGTCAATGACGAAATTCGCTTAAAGAGAGGACCAAGAGATGAAGCAACACTT 89515
QY 61 AAGCTTCACACTCCTCACTTAAACAGTCCCTTCAAACTTCCAGTCAACCTGAAGCTC 120
DB 89516 AAGCTTCACACTCCTCACTTAAACAGTCCCTTCAAACTTCCAGTCAACCTGAAGCTC 89575
QY 121 TTGAAGACACTGAATATATACACACAGCAGTGCAGTATGATGATACCTTAAGTCAAT 180
DB 89576 TTGAAGACACTGAATATATACACACAGCAGTGCAGTATGATGATACCTTAAGTCAAT 89635
QY 181 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCCCTAAAGAGAGCTTTGCT 240
DB 89636 ACCACAGGCGAGGGGCTGGGAGCGTACTCATCATCAACCCCTAAAGAGAGCTTTGCT 89695
QY 241 TCTCTCTTAAATAGATTACCTTACATTTTAAATGACCTGAATGTTAGTACTATA 300
DB 89696 TCTCTCTTAAATAGATTACCTTACATTTTAAATGACCTGAATGTTAGTACTATA 89755
QY 301 TCCCGCTACAAAAGGTAAACTTTTATATTTTATATTTTACTTACGCGCATTTGA 360
DB 89756 TCCCGCTACAAAAGGTAAACTTTTATATTTTATATTTTACTTACGCGCATTTGA 89815
QY 361 TATATATAAACATTTTACACATATGATTAAGTATTTTATTTTCTAATGCT 420
DB 89816 TATATATAAACATTTTACACATATGATTAAGTATTTTATTTTCTAATGCT 89875
QY 421 AGTCTTTCCCTGCTTAATGAAGCTT 448
DB 89876 AGTCTTTCCCTGCTTAATGAAGCTT 89903

RESULT 13
AC104439 197279 bp DNA linear PRI 20-JUN-2002
LOCUS
DEFINITION Homo sapiens chromosome 3 clone AP11-793B15, complete sequence.
ACCESSION AC104439
VERSION AC104439.2 GI:21490240
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Chniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 197279)
Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E. D.
Direct Submission
TITLE
JOURNAL Unpublished
2 (bases 1 to 197279)
REFERENCE Kaul, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 197279)
Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E. D.
Direct Submission
TITLE
JOURNAL Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jun 20, 2002 this sequence version replaced gi:17488621.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>

Contact: uwgchgs@u.washington.edu
Drafting Center: MUGSC

----- Project Information

Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)

----- Summary Statistics

Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; 108752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': RP11-91B8 (UMGC:bc0216) AC026349
3': CTD-2563A18 (UMGC:bc0730)

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phrap quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

BglII

ECORI

----- SegDerMap FngPrnt SegDerMap FngPrnt SegDerMap FngPrnt

2687	2617	8949	8586	8696	8661
6382	6410	2067	2160	6	<800
512	<800	7846	7940	2742	2803
449	<800	3734	3895	5376	5324
2602	2763	1334	1301	1493	1478
2590	2617	2287	2309	823	835
8313	8291	1814	1918	1962	2002
1711	1683	691	<800	2900	2954
9821	9472	5477	5348	1484	1478

516	<800	305	<800	1005	995
8587	8291	25245	25541	1181	1171
7446	7581	3988	4121	18560	19002
2088	2075	1633	1598	3603	3579
2509	2617	631	<800	4943	5076
3319	3501	90	<800	3239	3241
26	<800	402	<800	953	995
925	933	3350	3490	1621	1615
98	<800	4577	4515	6827	6900
6409	6410	1229	1183	79	<800
1383	1376	4221	4331	16418	16263
16048	15829	3980	4121	3361	3241
1876	1877	2548	2497	872	881
4169	4068	674	<800	4220	4193
1674	1683	2332	2309	2848	2803
52	<800	11445	11045	2283	2318
5227	5082	5692	5632	3211	3241
15464	15829	1385	1414	4615	4632
14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3356	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478

* 129484 131747: contig of 2264 bp in length
 * 131748 131847: gap of 100 bp
 * 131848 132316: contig of 469 bp in length
 * 132317 132416: gap of 100 bp
 * 132417 134455: contig of 2039 bp in length
 * 134456 134555: gap of 100 bp
 * 134556 135527: contig of 972 bp in length
 * 135528 135627: gap of 100 bp
 * 135628 189051: contig of 53424 bp in length
 * 189052 189151: gap of 100 bp
 * 189152 189476: contig of 325 bp in length
 * 189477 189576: gap of 100 bp
 * 189577 191375: contig of 1799 bp in length
 * 191376 191475: gap of 100 bp
 * 191476 201473: contig of 9998 bp in length
 * 201474 201573: gap of 100 bp
 * 201574 202307: contig of 734 bp in length
 * 202308 202407: gap of 100 bp
 * 202408 204878: contig of 2471 bp in length
 * 204879 204978: gap of 100 bp
 * 204979 213531: contig of 8553 bp in length
 * 213532 213631: gap of 100 bp
 * 213632 218109: contig of 4478 bp in length
 * 218110 218209: gap of 100 bp
 * 218210 219800: contig of 1591 bp in length
 * 219801 219900: gap of 100 bp
 * 219901 220965: contig of 1065 bp in length.

FEATURES

SOURCE

1. 220965
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="3"
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ORIGIN

Query Match 100.0%; Score 448; DB 14; Length 220965;
 Best Local Similarity 100.0%; Pred. No. 9.5e-84;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAATGAGAAATTCCTTAAGAGAGAGACCAAGAGATGAGCAACACATT 60
 DB 141329 TAGGTCAATGAGAAATTCCTTAAGAGAGAGACCAAGAGATGAGCAACACATT 141388
 QY 61 AAGCTTCCACACTCACTCTTAAACAGTCTTCAACTTCCAGTGCACACTGAAGCTC 120
 DB 141389 AAGCTTCCACACTCACTCTTAAACAGTCTTCAACTTCCAGTGCACACTGAAGCTC 141448
 QY 121 TTGAAGACACGTAATATATACACACAGCAGTAGAGATGATGATGACCTAAGGCTATT 180
 DB 141449 TTGAAGACACGTAATATATACACACAGCAGTAGAGATGATGATGACCTAAGGCTATT 141508
 QY 181 ACCACAGGCGCAGGGGCTGGGCGACGCTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 240
 DB 141509 ACCACAGGCGCAGGGGCTGGGCGACGCTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 141568
 QY 241 TCTCTCTCTAAATGAGTATACCTTAAATGAGCTGAAATGTTAGATGTTACTATTA 300
 DB 141569 TCTCTCTCTAAATGAGTATACCTTAAATGAGCTGAAATGTTAGATGTTACTATTA 141628
 QY 301 TGGCCCTCAAAAGGTAAAGCTTTTATATTATTAATTAACCTTCAAGCGCTATTGTA 360
 DB 141629 TGGCCCTCAAAAGGTAAAGCTTTTATATTATTAATTAACCTTCAAGCGCTATTGTA 141688
 QY 361 TATTAATATAACATTTTCAACATATCAATTAAGTTAACTATTATTTTCTATATGCGCT 420
 DB 141689 TATTAATATAACATTTTCAACATATCAATTAAGTTAACTATTATTTTCTATATGCGCT 141748
 QY 421 AGTTCTTTCCTGCTTAAATGAAAGCTT 448
 DB 141749 AGTTCTTTCCTGCTTAAATGAAAGCTT 141776

RESULT 15
AK123050
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK123050 1913 bp mRNA linear PRI 30-JAN-2004
 Homo sapiens CDNA FL141055.f1s; clone S1NOV2000601, highly similar
 to C-C GEMOKINE RECEPTOR TYR3 3.
 AK123050
 AK123050.1 GI:34528507
 oligo capsing; file (full insert sequence).
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 Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
AUTHORS

1. Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
 Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
 Sekine, M., Ohtsuka, S., Yoshioka, Y., Yoshikawa, T., Tanaka, T.,
 Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
 Nagahashi, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
 Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Kandaki, K., Yokoi, T., Furuya, T.,
 Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
 Tanikawa, M., Yamazaki, M., Nimomiya, K., Ishida, T., Yamashita, H.,
 Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
 Hirooka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
 Yosida, M., Hoshino, T., Kusano, Y., Kanehori, K., Takahashi-Fujii, A.,
 Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
 Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
 Sasaki, N., Aotsuka, S., Yoshioka, Y., Watanabe, H., Ichihara, T.,
 Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
 Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mitoguchi, H.,
 Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
 Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
 Tashiro, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y.,
 Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
 Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
 Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
 Nakajima, Y., Mizuno, T., Moritaga, M., Sasaki, M., Togaishi, T.,
 Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
 Nagase, T., Nomura, N., Kikuchi, H., Maehuo, Y., Yamashita, R.,
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Iisago, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length
 human cDNAs
 Nat. Genet. 36 (1), 40-45 (2004)
 14702039

JOURNAL
PUBMED
REFERENCE
AUTHORS

Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
 Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
 Yoshikawa, Y., Matsumura, K., Moriya, S., Chiba, E., Momiyama, H.,
 Onogawa, S., Kaeriyama, S., Satoh, N., Matsumura, H., Takahashi, R.,
 Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
 Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
 Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
 Kawai, H., Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
 Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
 Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
 Nagahashi, K., Maehuo, Y., Nagai, K. and Iisago, T.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 1913)

JOURNAL
REFERENCE
AUTHORS

Iisago, T. and Yamamoto, J.
 Direct Submission
 Submitted (15-JUN-2003) Takao Iisago, FUJ Project (HRI Team); 2-6-7
 Kazusa-Kametani, Kiserazu, Chiba 292-0818, Japan
 (E-mail: genomic@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan

COMMENT

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 07:05:07 ; Search time 668.111 Seconds
(without alignments)
3912.475 Million cell updates/sec

Title: US-10-767-521-3

Perfect score: 3586
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Scoring table: IDENTITY NUC
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Searched: 4637609 seqs, 364468668 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344.2	9.6	1915	7	US-11-068-686-3 Sequence 3, Appl1
2	319.2	8.9	2613	6	US-10-750-185-39572 Sequence 39572, A
3	319.2	8.9	2613	6	US-10-750-623-39572 Sequence 39572, A
4	211.4	5.9	187745	7	US-11-121-086-83 Sequence 83, Appl1
5	209	5.8	215308	6	US-11-121-086-77 Sequence 77, Appl1
6	208.2	5.8	256448	7	US-10-995-561-13369 Sequence 13369, A
7	208.2	5.8	235033	7	US-11-157-389-1 Sequence 1, Appl1
8	206.8	5.8	171162	7	US-11-112-908-38 Sequence 38, Appl1
9	206.4	5.8	130472	6	US-10-995-561-13312 Sequence 13312, A
10	204.2	5.7	246960	7	US-11-121-086-8 Sequence 8, Appl1
11	204.2	5.7	1080000	6	US-10-928-446A-1 Sequence 181, App
12	204.2	5.7	1080000	6	US-10-928-446A-181 Sequence 181, App
13	204.2	5.7	1080000	6	US-10-928-446A-183 Sequence 183, App
14	204.2	5.7	1080000	6	US-10-928-446A-185 Sequence 185, App
15	204.2	5.7	1080000	6	US-10-928-446A-187 Sequence 187, App
16	204.2	5.7	1080000	6	US-10-928-446A-189 Sequence 189, App
17	204.2	5.7	1080000	6	US-10-928-446A-191 Sequence 191, App
18	204.2	5.7	1080000	6	US-10-928-446A-193 Sequence 193, App
19	204.2	5.7	1080000	6	US-10-928-446A-195 Sequence 195, App
20	204.2	5.7	1080000	6	US-10-928-446A-197 Sequence 197, App
21	204.2	5.7	1080000	6	US-10-928-446A-199 Sequence 199, App
22	204.2	5.7	1080000	6	US-10-928-446A-201 Sequence 201, App
23	203.4	5.7	165156	6	US-10-995-561-13304 Sequence 13304, A

C 24	202.6	5.6	115935	6	US-10-775-169-241 Sequence 241, App
C 25	202.6	5.6	162289	7	US-11-121-086-20 Sequence 20, Appl
C 26	202.6	5.6	387780	6	US-10-995-561-13259 Sequence 13259, A
C 27	202.2	5.6	44848	7	US-11-106-672A-42 Sequence 42, Appl
C 28	201.8	5.6	319608	7	US-11-145-703-1 Sequence 1, Appl1
C 29	201.4	5.6	5982	7	US-11-034-771-1 Sequence 13294, A
C 30	201.4	5.6	15804	6	US-10-995-561-13294 Sequence 13294, A
C 31	201.4	5.6	24446	6	US-10-995-561-13436 Sequence 27, Appl
C 32	201.4	5.6	153142	7	US-11-121-086-27 Sequence 2, Appl1
C 33	201.4	5.6	191684	7	US-11-121-086-2 Sequence 20, Appl
C 34	201.2	5.6	191331	7	US-11-112-908-20 Sequence 9, Appl1
C 35	201.2	5.6	196200	7	US-11-121-086-9 Sequence 8, Appl1
C 36	201.2	5.6	246960	7	US-11-121-086-8 Sequence 14, Appl
C 37	201	5.6	5515	6	US-10-517-605-14 Sequence 2, Appl1
C 38	201	5.6	5515	7	US-11-055-309A-2 Sequence 13513, A
C 39	201	5.6	40000	6	US-10-995-561-13513 Sequence 40, Appl
C 40	201	5.6	180862	7	US-11-112-908-40 Sequence 13331, A
C 41	200.8	5.6	98716	6	US-10-995-561-13331 Sequence 24, Appl
C 42	200.8	5.6	150314	7	US-11-112-908-24 Sequence 61, Appl
C 43	200.8	5.6	159497	7	US-11-112-908-61 Sequence 60, Appl
C 44	200.8	5.6	171427	7	US-11-112-908-60 Sequence 2, Appl1
C 45	200.6	5.6	237326	7	US-11-157-389-2

ALIGNMENTS

RESULT 1
US-11-068-686-3
; Sequence 3, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Garstein, Murray & Borum
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 362..1426
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B polynucleotide and amino acid

QY	2717	AGTAAACCTAACTAATGCTGCTTAATATTTGAATATATATGTAATGTAATCTAGTGAT	2776
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Db	1422	-----	1423
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QY	3017	AAATTTACTTAAATTTCTTCAAGTTCAATTTCCCACTTA-----ACTTAATGAAATGCT	3070
Db	1314	TCCCTATTAAATTTCTTTTGAGGTTCAATTTCCCACTTACTGATATTTTAAATTTTGCAAT	1255
QY	3071	CATCATTAATGGGGCCCTGAGAGACATTAATCTGTAATGTAATGTAATCATTTGTTATTA	3130
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Db	911	ATCTGATACACTTTTGAATTAATGCTGAATAATGTAAGCT--ATTATTCGCTGTG	854
QY	3483	TCTTTGTGTGAGTACATGAATTAATCACTGTGTGTGTTTTTCAGAGATGATTAATCTTCA	3542
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; Sequence 39572, Application US/10750623			
; Publication No. US20050287531A1			
; GENERAL INFORMATION:			
; APPLICANT: NMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			

APPLICANT: FANTIN, Dennis	TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS	
FILE REFERENCE: MW11100-1		
CURRENT APPLICATION NUMBER: US/10/750,623		
CURRENT FILING DATE: 2003-12-31		
PRIOR APPLICATION NUMBER: US 60/437,482		
PRIOR FILING DATE: 2002-12-31		
NUMBER OF SEQ ID NOS: 64922		
SOFTWARE: PatentIn version 3.1		
SEQ ID NO 39572		
LENGTH: 2613		
TYPE: DNA		
ORGANISM: Bovine	19866881243305	
US-10-750-623--39572		
Query Match	8.9%; Score 319.2; DB 6; Length 2613;	
Best Local Similarity	60.0%; Pred. No. 1.9e-59;	
Matches 1251, Conservative	0; Mismatches 578; Indels 255; Gaps 33;	
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QY	1598 CTGACGAAAATTAGTAA-----TTTTTAAAGTTTGAACCTGTTTTAAATCACTTG	1653
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QY	1554 GAGAAAAAGAAAATTAATCAAAATTAATACGTGAATACAGCTACTATACCTTGT	1713
DB	2495 GAG--AAAAGAAAATAATTAATTAATTAATGATGATGAGGCTC-----	2449
QY	1714 CTCGAGATTAAGAGTCTGTCTTTCTTCTCTTGAATGCTGAAGTGAAGAGCACT	1773
DB	2448 -----TTTCACTTGCCTTAAACATTAAGTTTGAAGAGATCT	2409
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DB	2408 CTCATGACCGAAAATGATATACAGACCAATGATGGTACTTTTCTCAGCTGCTG----	2353
QY	1832 TTVGATTAATGCTATTAATGAATAGATGCTATG--GAGCACACAAACCAATTTGTC	1890
DB	2352 -TGATTAATGCAATGGGAATTTTTTAAAGCTGTGAATCATTAATGATCAGTTGCTAC	2294
QY	1891 TCACTCCATTTCTCTCTCAAAAGCTGGAATGTCCTATGATCAATGAGGAGATGTA	1950
DB	2293 TCAATTCATTTTAACTCGAAGGCTGAAATGATCATGATTAATGATGAATGAGCA	2234
QY	1951 GGAACGACCCATGAAAAGATCAACAGTTCACACCCAAAGGACCTTA--TTTTCTTAAT	2009
DB	2233 GGCGAGACTTATGAAATGAT--CAAGTCTATCCAAAGGCTCTACCTTTTCCGAT	2177
QY	2010 TTCAATTTAAATGCTCTTAATTTGCTTTCTTTCAATTCCTGCTCTAC--AGTTTTAC	2067
DB	2176 TTCAATGGAACCACTCTCATTCGCTTTTCTTCACTCTGCTTTTCAACATACAGTTT	2114
QY	2068 AGCTTTTCTGCTTTCAATGTAATCAATCACTCATTTTCTCATCAACACC	2122
DB	2116 TTTCTTTTCTAGTTTAAATATGATCTCATGTAGCTCTCTGATTTGATGTCACCAAT	2057
QY	2128 CAATGAC-----CAATGTCCTCATTTGATTAAGTAAGAGGCTCTGATTAAG	2187
DB	2056 CAATGGGTGCTACATGATCTTTATTTTGAATGAAATACAGGCTCAGAGTTAAG	1997
QY	2183 GGCTTTGTCAGGACGACGCTG-----AAGGCGCTAAGACTGCTCCATTTCCATCT	2236
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RESULT 8
US-11-112-908-38/c
; Sequence 38, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112, 908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564, 758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575, 978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631, 702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633, 826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

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[illegible]

QY	1297	TGGCTTGAATCTCGGGCTCAGGTAGACCTCCACACTGGGGCCCTCCAAAGTACTGGAT	1356
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RESULT 9
US-10-995-561-13312
; Sequence 13312, Application US/10995561
; Publication NO. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13312
; LENGTH: 130472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13312

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[illegible]

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RESULT 10
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, TIM S.
; APPLICANT: COULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3

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SEQ ID NO 8
LENGTH: 246960
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-8

Query Match 5.7%; Score 204.4; DB 7; Length 246960;
Best Local Similarity 70.1%; Pred. No. 7.6e-34;
Matches 289; Conservative 0; Mismatches 121; Indels 2; Gaps 1;

994 CTAATTTGATATTAAGTATTAACCTTGAATGAGCTGGGTAGACAGGTGAACCAATATC 1053
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QY 1054 AGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1113
DB 174407 TTTTTCCTTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 174466
QY 1114 CTGGCTG--TCGCCAGGCTGGAGTGCAGCGGCTGATCAAGTCACTGACGCTCAAC 1171
DB 174467 CTCGCTTCTTGGCCAGGCTGAGTGCAGTGGCGGATCTGCTCACTGCAACCTCGGC 174526
QY 1172 CTTTAGGCTCAGGAGATTTCTCCACCTCAGCCCCCAAGTATGTTGGACACAGATATG 1231
DB 174527 CTCACAGGTTCAGCAATTTCTGCTCCTCAGCCTCAAGTAGCTGGGATTAACGGCAG 174586
QY 1232 CGCCACCATGCTGGCTAATTTCTAATTTTGTATGATAGATGATCTCATATATGTC 1291
DB 174587 TGCCAGCATGCTGCTGATATTTTGTATTTATGATAGACAGAGTTTCAACATCTTGT 174646
QY 1292 CAGGCTGGCTGATATTCCTGGGCTCAGGTGAGCTCCCACTGGGCTCCCAAGTACT 1351
DB 174647 CAGGCTGGCTGATATTCCTGGGCTCAGGTGAGTCAACCGGCTCGCTCCCAAGTGT 174706
QY 1352 GGGATTACAGCATGAGCCAGAGTCCCTGCGCCATATGATTTCTGTCTC 1403
DB 174707 GGGATTACAGCATGAGTCACTGCTGCCAGCCCAAGTAACTTCTCTCTC 174758

RESULT 11
US-10-928-446A-1
Sequence 1, Application US/10928446A
Publication No. US20050277123A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
TITLE OF INVENTION: VARIANTS OF NED4L ASSOCIATED WITH HYPERTENSION AND
FILE REFERENCE: 0274-5785.1US
CURRENT APPLICATION NUMBER: US/10/928,446A
PRIOR FILING DATE: 2004-08-26
PRIOR APPLICATION NUMBER: 60/359,741
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1080000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (825270)
OTHER INFORMATION: the 'n' at position 825270 may be 'c' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (825234)
OTHER INFORMATION: the 'n' at position 825234 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (825401)
OTHER INFORMATION: the 'n' at position 825401 may be 'c' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (825428)

OTHER INFORMATION: the 'n' at position 825428 may be 'g' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (825473)
OTHER INFORMATION: the 'n' at position 825473 may be 'g' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (825765)
OTHER INFORMATION: a "c" may be deleted at this position
FEATURE:
NAME/KEY: allele
LOCATION: (825828)
OTHER INFORMATION: the 'n' at position 825828 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (826041)
OTHER INFORMATION: the 'n' at position 826041 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (826546)
OTHER INFORMATION: the 'n' at position 826546 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (826654)
OTHER INFORMATION: the 'n' at position 826654 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (826826)
OTHER INFORMATION: the 'n' at position 826826 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (827008)
OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (843118)
OTHER INFORMATION: the 'n' at position 843118 may be 'c' or 'c'
FEATURE:
NAME/KEY: allele
LOCATION: (871027)
OTHER INFORMATION: the 'n' at position 871027 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (871140)
OTHER INFORMATION: the 'n' at position 871140 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (871168)
OTHER INFORMATION: the 'n' at position 871168 may be 'c' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (872678)
OTHER INFORMATION: the 'n' at position 872678 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (872742)
OTHER INFORMATION: the 'n' at position 872742 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (925859)
OTHER INFORMATION: the 'n' at position 925859 may be 'c' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (993220)
OTHER INFORMATION: the 'n' at position 993220 may be 'c' or 't'

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1 FEATURE:
2 NAME/KEY: allele
3 LOCATION: (993254)
4 OTHER INFORMATION: the 'n' at position 993254 may be 'g' or 'a'
5 FEATURE:
6 NAME/KEY: allele
7 LOCATION: (1006462)
8 OTHER INFORMATION: the 'n' at position 1006462 may be 'c' or 't'
9 FEATURE:
10 NAME/KEY: allele
11 LOCATION: (1007820) ..(1007823)
12 OTHER INFORMATION: "ctc" may be deleted at this position
13 FEATURE:
14 NAME/KEY: allele
15 LOCATION: (1018038)
16 OTHER INFORMATION: the 'n' at position 1018038 may be 'a' or 'g'
17 FEATURE:
18 NAME/KEY: allele
19 LOCATION: (1018704)
20 OTHER INFORMATION: the 'n' at position 1018704 may be 'c' or 't'
21 FEATURE:
22 NAME/KEY: allele
23 LOCATION: (1018720) ..(1018720)
24 OTHER INFORMATION: "gtc" may be deleted at this position
25 FEATURE:
26 NAME/KEY: allele
27 LOCATION: (1026786)
28 OTHER INFORMATION: the 'n' at position 1026786 may be 'c' or 'a'
29 FEATURE:
30 NAME/KEY: allele
31 LOCATION: (1047134)
32 OTHER INFORMATION: the 'n' at position 1047134 may be 'a' or 'g'
33 FEATURE:
34 NAME/KEY: allele
35 LOCATION: (1047159)
36 OTHER INFORMATION: the 'n' at position 1047159 may be 'a' or 'g'
37 FEATURE:
38 NAME/KEY: allele
39 LOCATION: (1047378)
40 OTHER INFORMATION: the 'n' at position 1047378 may be 'c' or 't'
41 FEATURE:
42 NAME/KEY: allele
43 LOCATION: (1047739)
44 OTHER INFORMATION: the 'n' at position 1047739 may be 'a' or 'g'
45 FEATURE:
46 NAME/KEY: allele
47 LOCATION: (1050133) ..(1050137)
48 OTHER INFORMATION: "ctaaa" may be deleted at this position
49 FEATURE:
50 NAME/KEY: allele
51 LOCATION: (1050539)
52 OTHER INFORMATION: the 'n' at position 1050539 may be 'c' or 't'
53 FEATURE:
54 NAME/KEY: allele
55 LOCATION: (1062808)
56 OTHER INFORMATION: the 'n' at position 1062808 may be 'c' or 'g'
57 FEATURE:
58 NAME/KEY: allele
59 LOCATION: (1066392)
60 OTHER INFORMATION: the 'n' at position 1066392 may be 'a' or 'g'
61 FEATURE:
62 NAME/KEY: allele
63 LOCATION: (1073711)
64 OTHER INFORMATION: the 'n' at position 1073711 may be 'c' or 't'
65 JS-10-928-446A-1

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[illegible][illegible]

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RESULT 12
US-10-928-446A-181
: Sequence 181, Application US/10928446A
: Publication No. US20050277123A1
: GENERAL INFORMATION:
: APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
: TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
: FILE OF INVENTION: VIRAL BUDDING
: FILE REFERENCE: 0274-5785.1US
: CURRENT APPLICATION NUMBER: US/10/928,446A
: CURRENT FILING DATE: 2004-08-26
: PRIOR APPLICATION NUMBER: 60/359,741
: PRIOR FILING DATE: 2002-02-26
: NUMBER OF SEQ ID NOS: 202
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 181
: LENGTH: 1080000
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (826985)..(827008)
: FEATURE:
: OTHER INFORMATION: full exon 1 range is 826667-827008
: NAME/KEY: allele
: LOCATION: (827008)..(827008)
: OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (843242)..(843315)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (922549)..(922630)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (926021)..(926059)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (929123)..(929176)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (993104)..(993154)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (999547)..(999608)
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? FEATURE: CDS
? NAME/KEY: CDS
? LOCATION: (10645561)..(1064620)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1066207)..(1066314)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1067768)..(1067864)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1068609)..(1068681)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1073289)..(1073388)
? OTHER INFORMATION: full exon 30 range is 1073289-1075279
US-10-928-446A-181
Query Match          5.7%; Score 204.2; DB 6; Length 1080000;
Best Local Similarity 76.3%; Pred. No. 1.6e-33;
Matches 251; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY      1059 TTTAAATTTTTTAAATTTTTTAAATTTATTATTATTATTATTATTATTATTATTATTGAGATGAGCTGGC 1118
DB      960173 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAGACGTGCTCGCTC 960232
QY      1119 TGTGGCCCAAGGCTGAGAGTCGACGGCCGTGATCACAGTTCACTGCGAGCCTCAACTTTMG 1178
DB      960233 TGTGCCCAAGGCTGAGAGCGAGTGATGAGTCTAGCTCATCGCAACTCCACTTCCCG 960292
QY      1179 GCTCAAGGGAATTCCTCCCACTCAGCCCCCAAGTAGTAGGAGACAACGTATGCACC 1238
DB      960293 GTTCAAGGATTCCTCGCCTTAGCCTCTGAGTAGCTGGAGATTACAGGTGACGCCACC 960352
QY      1239 ATGCTGGCTAATTTCTAATTTTTTTGTAAGATGAGATCTCAATAATTGTCAAGCTG 1298
DB      960353 ACACCTGGCTAATTTCTGTATTTTTTGTAGAAGAGCGGGTTTACCATGTTGTCAAGCTG 960412
QY      1299 GTCTTGAATTCCTGGGCTCAGGTGAGCTCCCACTGGGCGCTCCCAAAGTACTGGGATTA 1358
DB      960413 GTCTCAAACTCTGACCTCAGGTGATCCACCGCGCTCGCCCTCCCAAAGTGTGGGATTA 960472
QY      1359 CAGGCATGAGCGCAAGTCTCCCTGCCCATTA 1387
DB      960473 CAGGCGTAGCCACCATGCCAGCCCATTA 960501
RESULT 13
US-10-928-446A-183
? Sequence 183, Application US/10928446A
? Publication No. US20050277123A1
? GENERAL INFORMATION:
? APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
? TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
? TITLE OF INVENTION: VIRAL BUDDING
? FILE REFERENCE: 0274-5785.1US
? CURRENT APPLICATION NUMBER: US/10/928.446A
? PRIOR FILING DATE: 2004-08-26
? PRIOR APPLICATION NUMBER: 60/359,741
? NUMBER OF SEQ ID NOS: 202
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 183
? LENGTH: 1080000
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS

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1 LOCATION: (826985)..(827017)
2 FEATURE:
3 OTHER INFORMATION: full exon 1 range is 826667-827008
4
5 FEATURE:
6 NAME/KEY: CDS
7 LOCATION: (843242)..(843315)
8 OTHER INFORMATION: exon
9
10 FEATURE:
11 NAME/KEY: CDS
12 LOCATION: (922549)..(922630)
13 OTHER INFORMATION: exon
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (926021)..(926059)
17 OTHER INFORMATION: exon
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (929123)..(929176)
21 OTHER INFORMATION: exon
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (931104)..(931154)
25 OTHER INFORMATION: exon
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: (939547)..(939608)
29 OTHER INFORMATION: exon
30 FEATURE:
31 NAME/KEY: CDS
32 LOCATION: (1000354)..(1000456)
33 OTHER INFORMATION: exon
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: (1002118)..(1002284)
37 OTHER INFORMATION: exon
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: (1006117)..(1006249)
41 OTHER INFORMATION: exon
42 FEATURE:
43 NAME/KEY: CDS
44 LOCATION: (1007860)..(1008036)
45 OTHER INFORMATION: exon
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: (1010940)..(1011014)
49 OTHER INFORMATION: exon
50 FEATURE:
51 NAME/KEY: CDS
52 LOCATION: (1018160)..(1018291)
53 OTHER INFORMATION: exon
54 FEATURE:
55 NAME/KEY: CDS
56 LOCATION: (1018800)..(1018919)
57 OTHER INFORMATION: exon
58 FEATURE:
59 NAME/KEY: CDS
60 LOCATION: (1020028)..(1020225)
61 OTHER INFORMATION: exon
62 FEATURE:
63 NAME/KEY: CDS
64 LOCATION: (1026659)..(1026736)
65 OTHER INFORMATION: exon
66 FEATURE:
67 NAME/KEY: CDS
68 LOCATION: (1028113)..(1028167)
69 OTHER INFORMATION: exon
70 FEATURE:
71 NAME/KEY: CDS
72 LOCATION: (1034316)..(1034374)
73 OTHER INFORMATION: exon
74 FEATURE:
75 NAME/KEY: CDS

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/ LOCATION: (1041390)..(1041455)
/ OTHER INFORMATION: exon
/ FEATURE:
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/ LOCATION: (1043121)..(1043350)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1044868)..(1044989)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1047519)..(1047589)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1050296)..(1050391)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1060368)..(1060441)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1062648)..(1062708)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1064561)..(1064620)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1066207)..(1066314)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1067768)..(1067864)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1068609)..(1068681)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1073289)..(1073388)
/ OTHER INFORMATION: full exon 30 range is 1073289-1075279
/
/ US-10-928-446A-183

```

[illegible]

0Y 1359 CAGGCATGAGCCCAAGTCCCTGCCCATTA 1387
Db 960473 CAGGCGTGAGCCACCATGCCAGCCCATTA 960501
RESULT 14
US-10-928-446A-185
Sequence 185, Application US/10928446A
Publication No. US20050277123A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
TITLE OF INVENTION: VARIANTS OF NEDP4L ASSOCIATED WITH HYPERTENSION AND
TITLE OF INVENTION: VIRAL BUDDING
FILE REFERENCE: 0274-5785..1US
CURRENT APPLICATION NUMBER: US/10/928,446A
CURRENT FILING DATE: 2004-08-26
PRIOR APPLICATION NUMBER: 60/359,741
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 202
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 185
LENGTH: 1080000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (722487)..(722534)
FEATURE:
OTHER INFORMATION: full length exon 1 range is 722213-722514
FEATURE:
NAME/KEY: CDS
LOCATION: (843242)..(843315)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (922549)..(922630)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (926021)..(926059)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (929123)..(929176)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (993104)..(993154)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (999547)..(999608)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION: exon
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NAME/KEY: CDS
LOCATION: (1002118)..(1002284)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION: exon
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LOCATION: (1010940)..(1011014)
OTHER INFORMATION: exon

FEATURE:
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NAME/KEY: CDS
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OTHER INFORMATION: exon
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NAME/KEY: CDS
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FEATURE:
NAME/KEY: CDS
LOCATION: (1044868)..(1044989)
OTHER INFORMATION: exon
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NAME/KEY: CDS
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OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION: exon
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NAME/KEY: CDS
LOCATION: (1066207)..(1066314)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1067768)..(1067864)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1068609)..(1068681)
OTHER INFORMATION: exon
FEATURE:
NAME/KEY: CDS
LOCATION: (1073289)..(1073388)
OTHER INFORMATION: full length exon 30 range is 1073289-1075279

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 7, 2006, 06:18:20 ; Search time 2602.82 seconds
(without alignments)
11393.018 Million cell updates/sec

Title: US-10-767-521-3
Perfect score: 3586
Sequence: 1 ggcaccctaccctcccatc.....ctaccagggagaagtga 3586

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3586	100.0	3586	US-09-922-895-3	Sequence 3, Appl1
2	3586	100.0	3586	US-10-767-521-3	Sequence 3, Appl1
3	3494.4	97.4	5791	US-10-929-182-21	Sequence 21, Appl1
4	3494.4	97.4	5791	US-10-486-471-5	Sequence 5, Appl1
5	2406	67.1	7201	US-10-311-455-310	Sequence 310, Appl1
6	2271.8	63.4	7201	US-10-311-455-309	Sequence 309, Appl1
7	344.2	9.6	1915	US-10-106-623-3	Sequence 3, Appl1
8	344.2	9.6	1915	US-10-106-623-3	Sequence 3, Appl1
9	215.2	6.0	3771	US-09-925-065A-727856	Sequence 727856,
10	212.4	5.9	606	US-09-925-065A-804603	Sequence 804603,
11	212.2	5.9	582	US-09-925-065A-248133	Sequence 248133,
12	212.2	5.9	726	US-09-925-065A-923960	Sequence 923960,
13	211.8	5.9	13000	US-10-719-993-6920	Sequence 6920, App
14	211.8	5.9	54701	US-10-087-192-946	Sequence 946, App
15	211.8	5.9	60316	US-10-719-993-6833	Sequence 6833, App
16	211.4	5.9	1418	US-09-925-065A-53249	Sequence 53249, A
17	211.4	5.9	1418	US-09-925-065A-53250	Sequence 53250, A
18	211.4	5.9	1418	US-09-925-065A-53251	Sequence 53251, A
19	211.4	5.9	1418	US-09-925-065A-53252	Sequence 53252, A
20	211.2	5.9	606	US-09-925-065A-857329	Sequence 857329,
21	211.2	5.9	606	US-09-925-065A-857330	Sequence 857330,
22	211	5.9	582	US-09-925-065A-248131	Sequence 248131,
23	211	5.9	582	US-09-925-065A-248134	Sequence 248134,

24	210.8	5.9	1234	4	US-09-925-065A-696705	Sequence 696705,
25	210.6	5.9	582	4	US-09-925-065A-248132	Sequence 248132,
26	210.6	5.9	102790	7	US-10-367-094-163	Sequence 163, App
27	210.6	5.9	160361	7	US-10-235-192A-35	Sequence 35, Appl
28	210.4	5.9	787	4	US-09-925-065A-936523	Sequence 936523,
29	210.2	5.9	631	4	US-09-925-065A-169305	Sequence 169305,
30	210.2	5.9	168821	5	US-10-087-192-622	Sequence 622, App
31	209.8	5.9	631	4	US-09-925-065A-169304	Sequence 169304,
32	209.8	5.9	657	4	US-09-925-065A-925251	Sequence 925251,
33	209.6	5.8	210	4	US-09-925-065A-349513	Sequence 349513,
34	209.6	5.8	155572	9	US-10-981-277-30	Sequence 30, Appl
35	209.2	5.8	787	4	US-09-925-065A-936524	Sequence 936524,
36	209	5.8	59215	9	US-10-472-923-3	Sequence 3, Appl1
37	208.8	5.8	746	4	US-09-925-065A-936526	Sequence 936526,
38	208.8	5.8	746	4	US-09-925-065A-936526	Sequence 936526,
39	208.8	5.8	787	4	US-09-925-065A-936525	Sequence 936525,
40	208.2	5.8	235033	5	US-10-301-844-1	Sequence 1, Appl1
41	208	5.8	612	4	US-09-925-065A-940151	Sequence 940151,
42	208	5.8	620	4	US-09-925-065A-926832	Sequence 926832,
43	207.4	5.8	652	5	US-10-027-632-14511	Sequence 14511, A
44	207.4	5.8	652	6	US-10-027-632-14511	Sequence 14511, A
45	206.4	5.8	119501	6	US-10-174-319-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-922-895-3
Sequence 3, Application US/09922895
Publication No. US20020192214A1
GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,895
FILING DATE: 06-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/847,296
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19634Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3586 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

2041 TCCATTCGCTGCTCCACAGATTTCACAGCTTTCTGCTTCAATGTGAATCACTACATA 2100
2101 CACTCCTATTTTCTCCATACCAACCCAGTGAATGAGTCTGCTTCTGATATTA 2160
2101 CACTCCTATTTTCTCCATACCAACCCAGTGAATGAGTCTGCTTCTGATATTA 2160
2161 GTAAAGAGGCTCTGCAATTAAGGGCTTGTCCAAAGGACGAGCTGAGAGGCTGAGACT 2220
2161 GTAAAGAGGCTCTGCAATTAAGGGCTTGTCCAAAGGACGAGCTGAGAGGCTGAGACT 2220
2221 GGCCTCATTTTCATCTATTTCTCATCTGACTTGAACCCCAATCCCAATGAGGAG 2280
2221 GGCCTCATTTTCATCTATTTCTCATCTGACTTGAACCCCAATCCCAATGAGGAG 2280
2281 CCTCATTTTCATCTATTTCTCATCTGACTTGAACCCCAATCCCAATGAGGAG 2340
2281 CCTCATTTTCATCTATTTCTCATCTGACTTGAACCCCAATCCCAATGAGGAG 2340
2341 GTTATTTAAGCATTTCTCAGATTTTACCTTGAGAAATGCGCATGAGCTGATATTCACATC 2400
2341 GTTATTTAAGCATTTCTCAGATTTTACCTTGAGAAATGCGCATGAGCTGATATTCACATC 2400
2401 TTCACTCTTGTCT 2460
2401 TTCACTCTTGTCT 2460
2461 AGTGCATGCTTACCTGCT 2520
2461 AGTGCATGCTTACCTGCT 2520
2521 TTTCCACGGAAGTCTATATCTCAAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
2521 TTTCCACGGAAGTCTATATCTCAAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
2581 AGAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTGTG 2640
2581 AGAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTGTG 2640
2641 ATGGAAGGCTCCAGGGGTTTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATG 2700
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2701 GGGGCAAGAAAAGAAAGTAACTTAATGCTGCTTAAATGATGATGATGATGATGATGATGATG 2760
2701 GGGGCAAGAAAAGAAAGTAACTTAATGCTGCTTAAATGATGATGATGATGATGATGATGATG 2760
2761 GTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
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2941 GACAGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
2941 GACAGAGAAATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
3001 TTAAAGGATTTTGAACAAATTAATTAATTTTCAAGGTTCAATTTTCCCATTAATTAATTA 3060
3001 TTAAAGGATTTTGAACAAATTAATTAATTTTCAAGGTTCAATTTTCCCATTAATTAATTA 3060
3061 ATGAATGCTCATCTATTTATGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
3061 ATGAATGCTCATCTATTTATGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
3121 ATTTGATTTATTTATTAATTAATTTTGTCTTTTAAATGATGATGATGATGATGATGATGATG 3180
3121 ATTTGATTTATTTATTAATTAATTTTGTCTTTTAAATGATGATGATGATGATGATGATGATG 3180
3121 ATTTGATTTATTTATTAATTAATTTTGTCTTTTAAATGATGATGATGATGATGATGATGATG 3180

3181 TAACTGTAAACATATAATGCAAAATGCGTAAAGACAGTATGATATATATATATAT 3240
3181 TAACTGTAAACATATAATGCAAAATGCGTAAAGACAGTATGATATATATATATATAT 3240
3241 TATATTTAT 3300
3241 TATATTTAT 3300
3301 TATATTTAT 3360
3301 TATATTTAT 3360
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3361 ATGCGGCTCATGCTAATCTTGAAGGCTTCAAGCTCTTCTCTCTCTCTCTCTCTCTCTCTCT 3420
3421 ACCCTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTGATATCAATGTG 3480
3421 ACCCTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTGATATCAATGTG 3480
3481 CATCTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3540
3481 CATCTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3540
3541 CATTTGGGATTTGATTTTCTTCTTCTATCAAGGAGAGTGA 3586
3541 CATTTGGGATTTGATTTTCTTCTTCTATCAAGGAGAGTGA 3586

US-10-767-521-3
RESULT 2
US-10-767-521-3
Sequence 3, Application US/10767521
Public Access No. US20050033024A1
GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: DEMARTINO, JULIE A.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SPRINGER, MARTIN J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING EOSINOPHIL BOTRAXIN
FILE REFERENCE: 19634YDACA
CURRENT APPLICATION NUMBER: US/10/767,521
PRIORITY FILING DATE: 2004-01-29
PRIORITY FILING DATE: 60/016,158
PRIORITY FILING DATE: 1996-04-26
PRIORITY FILING DATE: 09/922,895
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 3586
TYPE: DNA
ORGANISM: Human
US-10-767-521-3

Query Match 100.0%; Score 3586; DB 8; Length 3586;
Best Local Similarity 100.0%; Pct. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAATCCCTAATCTTCCCATCAAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
1 GGAATCCCTAATCTTCCCATCAAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
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61 CCCCCAAGAAATGCTCTCCCTGTGGGCACTTCTTACAGATGAGAGGAGGAGGAGGAGGAGGAGG 120
61 CCCCCAAGAAATGCTCTCCCTGTGGGCACTTCTTACAGATGAGAGGAGGAGGAGGAGGAGGAGG 120
61 CCCCCAAGAAATGCTCTCCCTGTGGGCACTTCTTACAGATGAGAGGAGGAGGAGGAGGAGGAGG 120
121 AAGTTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
121 AAGTTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
181 GTTCATGCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

181 GTTCATGCGATGGGAGGAGTCAAGAGCAGACGCTTGCTCAGTGCCTACAGTGA 240
241 GGAAGAGTGAACACCTGGGCGAGGGGCGCTGGTGAAGGCTATGATTAACGA 300
241 GGAAGAGTGAACACCTGGGCGAGGGGCGCTGGTGAAGGCTATGATTAACGA 300
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301 GAGGCTCTCATTCAGTCCAGGCAAGAGAGCTAAGATGAATATCCTATGATTAATAGC 360
361 TACAAACCAACACAGAGGTTCCAGAAAAGGCTCAGGCTTGAACCAAGTCACCCCAC 420
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421 TCAGAGACACAGATCTAATTAATCAAGGACCAACAGAGAGAGGAAACCCCTTCCCA 480
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481 CTCTGCCCCATGCTCAAGTTGATGAGGCTTCTCTCAGATCTCTGCCACCATCTTGA 540
481 CTCTGCCCCATGCTCAAGTTGATGAGGCTTCTCTCAGATCTCTGCCACCATCTTGA 540
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901 GTTCTTTCTTAATGTTCTTACTTATTTAGATTAACCTTACCTTATCCCAAAATGTA 960
901 GTTCTTTCTTAATGTTCTTACTTATTTAGATTAACCTTACCTTATCCCAAAATGTA 960
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1021 ATTGAAGCTGGGTAGACAGGTGAAAACATATCAGGTTTTTAAATTTTAAATTTA 1080
1081 ATTGAATTTAATTTATTTTATTTTATGATGAGTCTGGCTGTGCCCAAGCTGAGTGC 1140
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1561 TGAATTAACATGATTAATTAAGACATACCTCAACTGAGCAAACTTAATTTA 1620
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1681 TTAACGATGAATACAGGCTACTATACCTTTGTTCTCAAGATTAAGCTGTTCTTT 1740
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1741 CTTCCTTTATGATGCTGAAGTGAAGAGACATCTGTGATTTGTAGTGTATCTGAACA 1800
1801 AATGTATTTTTTTCTCAGCTGCTATGAGATTTGATTAATGATTAATGAATATG 1860
1801 AATGTATTTTTTTCTCAGCTGCTATGAGATTTGATTAATGATTAATGAATATG 1860
1861 TGATGGAGACACAAACCAATTTGTTCTCAGTCAATTTCTCTCAAAAGCTGGA 1920
1861 TGATGGAGACACAAACCAATTTGTTCTCAGTCAATTTCTCTCAAAAGCTGGA 1920
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1981 TCCACCCAAAGGACCTATTTTCTCAATTTGATTTGAATGAGCTTAAATGCTCTCT 2040
1981 TCCACCCAAAGGACCTATTTTCTCAATTTGATTTGAATGAGCTTAAATGCTCTCT 2040
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QY	2401	TTCAACCCCTGGTCCCTTCCCTCCAGAAAAGAAAAGTCACTGGAAAGCCCTCGAGAACT	2460
Dp	2401	TTCAACCCCTGGTCCCTTCCCTCCAGAAAAGAAAAGTCACTGGAAAGCCCTCGAGAACT	2460
QY	2461	AGTGCATGGCTTAACTGTCTCTTCCATGACTCTGGCTTATCTGTCTTATTTTCTCTCT	2520
Dp	2461	AGTGCATGGCTTAACTGTCTCTTCCATGACTCTGGCTTATCTGTCTTATTTTCTCTCT	2520
QY	2511	TTTTCACCGGAAGTCTATTAATCTCAAGAAAAGCAGGCACTGGGCTTCCTGGCCTTA	2580
Dp	2511	TTTTCACCGGAAGTCTATTAATCTCAAGAAAAGCAGGCACTGGGCTTCCTGGCCTTA	2580
QY	2581	AGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCGCTTACCCCTTGTG	2640
Dp	2581	AGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCGCTTACCCCTTGTG	2640
QY	2641	ATGAGAAAGCTCCAGGGGTTTGTCTTTTGACATGTTACAGGCGCTTAATCTGACATCACCA	2700
Dp	2641	ATGAGAAAGCTCCAGGGGTTTGTCTTTTGACATGTTACAGGCGCTTAATCTGACATCACCA	2700
QY	2701	GGGGCAAAAAGAAAAGTAACTTAACCTTAATGCTTATTAATGTAATTAATGTAATA	2760
Dp	2701	GGGGCAAAAAGAAAAGTAACTTAACCTTAATGCTTATTAATGTAATTAATGTAATA	2760
QY	2761	GTTAATTAATCTGTGANTGTACANTGTGTACAGCAAAAAGTGTATTTTTTTCACAGCTGCT	2820
Dp	2761	GTTAATTAATCTGTGANTGTACANTGTGTACAGCAAAAAGTGTATTTTTTTCACAGCTGCT	2820
QY	2821	GTGATTTGATTTATGCCAATTTTGAATTAAGAAATGCTGTTAAGACACACAGCGAGTTCC	2880
Dp	2821	GTGATTTGATTTATGCCAATTTTGAATTAAGAAATGCTGTTAAGACACACAGCGAGTTCC	2880
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Dp	2881	TCAAGTCCGTGACAAATTTTCAAAAGTTAAATTTAAAAATCACATCAATTTGAATCTAGT	2940
QY	2941	GACAGAGAAATGACATGATATAGACCTAAAGATCTAGCCCAATTTTATATTTACTTG	3000
Dp	2941	GACAGAGAAATGACATGATATAGACCTAAAGATCTAGCCCAATTTTATATTTACTTG	3000
QY	3001	TTAAGAGATTTTGAACAAATTAATCTAAATTTCTTCAAGGTTCAATTTCCCATTAATCTATA	3060
Dp	3001	TTAAGAGATTTTGAACAAATTAATCTAAATTTCTTCAAGGTTCAATTTCCCATTAATCTATA	3060
QY	3061	ATGAATGCTCATCTAATTAAGGGGCCCTGAGAAAGATTAATTAATCTGTAATGTAATATC	3120
Dp	3061	ATGAATGCTCATCTAATTAAGGGGCCCTGAGAAAGATTAATTAATCTGTAATGTAATATC	3120
QY	3121	ATTGTTATTAATTAATTAATCATATTTTGTCTTTAAATGATTAAGATTTTAAAGTAAATG	3180
Dp	3121	ATTGTTATTAATTAATTAATCATATTTTGTCTTTAAATGATTAAGATTTTAAAGTAAATG	3180
QY	3181	TAAATCTGTAACATTAATAATGCAAAATGCCGTAAAGACATGTAGAAATTAATTAAGATTAAT	3240
Dp	3181	TAAATCTGTAACATTAATAATGCAAAATGCCGTAAAGACATGTAGAAATTAATTAAGATTAAT	3240
QY	3241	TAAATGTTATCATTAATCTAGCTGTGTTTTTCTGTGTGTAATTTCTTCTTTAAATGCT	3300
Dp	3241	TAAATGTTATCATTAATCTAGCTGTGTTTTTCTGTGTGTAATTTCTTCTTTAAATGCT	3300
QY	3301	TACAGAAATCTGTAATCCCATTTCTTACACACACCCCAACAAATTTGCTGCTCTTTTCCC	3360
Dp	3301	TACAGAAATCTGTAATCCCATTTCTTACACACACCCCAACAAATTTGCTGCTCTTTTCCC	3360
QY	3361	ATGCGGATCATGCTTAATCTTGAAGCTTCAAGCTCTTCTCTTCTCAATCTTCTCTGGC	3420
Dp	3361	ATGCGGATCATGCTTAATCTTGAAGCTTCAAGCTCTTCTCTTCTCAATCTTCTCTGGC	3420
QY	3421	AACCTGTGATATGCCCTTTGAAATTCATGTTAAAGATCCCTAAGCTGTATACACATGAGG	3480
Dp	3421	AACCTGTGATATGCCCTTTGAAATTCATGTTAAAGATCCCTAAGCTGTATACACATGAGG	3480

Qy	3481	CATCTTGTGAGACATGATTAATCAACGGGTGTTTACGAAGATGATTATGCTT	3540
Db	3481	CATCTTGTGAGACATGATTAATCAACGGGTGTTTACGAAGATGATTATGCTT	3540
Qy	3541	CATTGGGAGATTGATTTTCTTCTTCATCACGGGAGAAAGTGA	3586
Db	3541	CATTGGGAGATTGATTTTCTTCTTCATCACGGGAGAAAGTGA	3586

RESULT 3

```

US-10-929-182-21
Sequence 21, Application US/10929182
Publication No. US20050064483A1
GENERAL INFORMATION:
APPLICANT: Zang, Jingwu
APPLICANT: Hong, Jian
TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
TITLE OF INVENTION: Multiple Sclerosis
PILS REFERENCE: HO-P02850S1
CURRENT APPLICATION NUMBER: US/10/929,182
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: US 60/498,731
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 5791
TYPE: DNA
ORGANISM: HUMAN
US-10-929-182-21

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Query match	97.4%	Score 3494.4;	DB 9;	Length 5791;
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Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

1 GGATCCCTACCTTCCCATCAGAGCTAGGGGCATGGAGCGCTCTCTGCTAAGATGGGA 60

Db 433 GGATCCCTACCTTCCCCATCAGAGCTAGGGGGCATGGAGCGCTCTCTGCTAAGATGGGA 492

61 CCCCAAGGAATGTCTCCCTGTGGGCACTTCCTTACCAGATGGATGGCCAGTCCGTT 120

Db 493 CCCCAGGAAATGTCCTCTGAGGCACTTCTTACCAGATGGGATGGCCAGTGCCT 552

121 AAGTGGTGGTCAGGCAAGAAAAGATGTAGTTGTACTCTGAGAGTCCCTGGTTT 180

DD 353 AA01.UG1UG1.AAGGAAHHHAAAHVAAV1.1.VA.VC.V1.AAAABV.1.CC1CCB.V1.V2

100

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RESULT 4
US-10-486-471-5
; Sequence 5, Application US/10486471
; Publication No. US20050101530A1
; GENERAL INFORMATION:
; APPLICANT: TOPISGEN PHARMACEUTICALS INC.
; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE
; FILE REFERENCE: 009953-0003
; CURRENT APPLICATION NUMBER: US/10/486,471
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/311,088
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5791

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4015)..(5082)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF247361
; DATABASE ENTRY DATE: 2002-06-26
; RELEVANT RESIDUES: (1)..(5791)
US-10-486-471-5

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Query Match 97.4%; Score 3494.4; DB 9; Length 5791;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

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QY	1020	GATTGAGCTGGGTGACAGGTTAAACCATACAGGTTTAAATTTTAAATTTTAAAT	1079
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QY	1680	ATTAACGCGTAATACAGGCTACTATACCTTTGTTCTCAGAAATTAAGAGCTTCTGTCCTT	1739
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QY	1860	CTGATGGAGACACACAACATTTGTTCTCAGTCACTATTTCTCTCAAAAGCCTGG	1919
Db	2287	CTGATGGAGACACACAACATTTGTTCTCAGTCACTATTTCTCTCAAAAGCCTGG	2346
QY	1920	AATGTGCATTTGATCAGTGGAGATGTACCTGACACAGCCATGAAAAGATCAACAG	1979

Db	2347	ATATGGCATTGATTCAGTGGGAGATGTACCTGGACAGACCCTAGAAAGATCAACAG	2406
Qy	1980	TTCCACCCAGAGGACCCCTATTTTTCCTAATTCATTGAAATGGCTTCTAATGTCTTC	2039
Db	2407	TTCCACCCAGAGGACCCCTATTTTTCCTAATTCATTGAAATGGCTTCTAATGTCTTC	2466
Qy	2040	TTTCAATTCGTGCTCCACACGAGTTTACAGCTTTTCGGTTTCAATGTGAATGCAT	2099
Db	2467	TTTCAATTCGTGCTCCACACGAGTTTACAGCTTTTTCGGTTTCAATGTGAATGCAT	2526
Qy	2100	ACACTCTCATTTTTCCTCATATCAACACCCCAAGTGAACCAATGTGCTCACCTTCGATATA	2159
Db	2527	ACACTCTCATTTTTCCTCATATCAACACCCCAAGTGAACCAATGTGCTCACCTTCGATATA	2586
Qy	2160	AGTAAAGGAGGCTCTGCATTAAAGGCTTGTCCAAAGCAGCAGCTGAGAGGCTTAGAC	2219
Db	2587	AGTAAAGGAGGCTCTGCATTAAAGGCTTGTTCAAAGCAGCAGCTGAGAGGCTTAGAC	2646
Qy	2220	TGGCTCCATTTCCATCTCTAATTCACCTGACTTTGACTACCCAGAACCCCAATGTGGG	2279
Db	2647	TGGCTCCATTTCCATCTCTAATTCACCTGACTTTGACTACCCAGAACCCCAATGTGGG	2706
Qy	2280	GGCTCAGATTCGATTCATTAATTTCTAATTAAGAACCAAAAACAATCCCGCATTTGGCCC	2339
Db	2707	GGCTCAGATTCGATTCATTAATTTCTAATTAAGAACCAAAAACAATCCCGCATTTGGCCC	2766
Qy	2340	AGTTATTAAGCATTTCTCAGATTTACCTTGAAATGCCATGGGCTGTATATTCAT	2399
Db	2767	AGTTATTAAGCATTTCTCAGATTTACCTTGAAATGCCATGGGCTGTATATTCAT	2826
Qy	2400	CTTCAACCTTGTCCCTTCCTCTTGAAAGGAGAAAGTCAGTTGGAATGCCCTCGAGGAC	2459
Db	2827	CTTCAACCTTGTCCCTTCCTCTTGAAAGGAGAAAGTCAGTTGGAATGCCCTCGAGGAC	2886
Qy	2460	TAGTSCATGGCTTAACTGTCCCTCCATGACCTCGCTTATCTGTTTCTAATTTCCCTCC	2519
Db	2887	TAGTSCATGGCTTAACTGTCCCTCCATGACCTCGCTTATCTGTTTCTAATTTCCCTCC	2946
Qy	2520	TTTTTCACCCGAGCTATATATCTCAGAAAGAGAGGCACTGGGCTTAGGGCTCTGGCCT	2579
Db	2947	TTTTTCACCCGAGCTATATATCTCAGAAAGAGAGGCACTGGGCTTAGGGCTCTGGCCT	3006
Qy	2580	AAGAAATTCAGATTCAGTGAAGAAATCCCATGACTGACCCCTCTGTACCCCTTGT	2639
Db	3007	AAGAAATTCAGATTCAGTGAAGAAATCCCATGACTGACCCCTCTGTACCCCTTGT	3066
Qy	2640	GATGAGAGAGCTCCGAGGGGTTTGCTTTTTCAGTTTACAGAGGCTTACTCAGATCAC	2699
Db	3067	GATGAGAGAGCTCCGAGGGGTTTGCTTTTTCAGTTTACAGAGGCTTACTCAGATCAC	3126
Qy	2700	AGGGGCAAGAAAGAAAGTAACCTAACTATGTGCTTATTAATGTAAATTTGTAT	2759
Db	3127	AGGGGCAAGAAAGAAAGTAACCTAACTATGTGCTTATTAATGTAAATTTGTAT	3186
Qy	2760	AGTTAATTACTGTGATGTGTACATGTGTAACTGACAAATGTGTATTTTTCACAGCTGC	2819
Db	3187	AGTTAATTACTGTGATGTGTACATGTGTAACTGACAAATGTGTATTTTTCACAGCTGC	3246
Qy	2820	TGTGATTTGATTAATGACATTTGGAATAAAGATGCTGTTAAGACACACAGCAGGTTCC	2879
Db	3247	TGTGATTTGATTAATGACATTTGGAATAAAGATGCTGTTAAGACACACAGCAGGTTCC	3306
Qy	2880	CTCAAGTCCGTGACAAATTTTTCAAAAGTAAATTTTAAATAATCACTATTTGATCTAG	2939
Db	3307	CTCAAGTCCGTGACAAATTTTTCAAAAGTAAATTTTAAATAATCACTATTTGATCTAG	3366
Qy	2940	TGACAGAGAAATGACATGTATGAGACTAAAGATCTAGCCCAATTTTATATTAATCTT	2999
Db	3367	TGACAGAGAAATGACATGTATGAGACTAAAGATCTAGCCCAATTTTATATTAATCTT	3426
Qy	3000	GTTAAGAGATTTTGAACAAATTAATTAATTTCTCAAGTCAATTTCCGCAATTAACAT	3059
Db	3427	GTTAAGAGATTTTGAACAAATTAATTAATTTCTCAAGTCAATTTCCGCAATTAACAT	3486

QY	1142	GGCGGATACAGTTCATCTGACGCTCCAACTCTCGAGCTCAAGGATTTCCCACTCA	1201
Db	4616	GACGTAATCACAAATTCACCTACCACTCAACTCTTCAAACTCAAAAATTTCCCACTCA	4557
QY	1202	GCCCCCAAGTAGTGGGACCAACAGTATGGGCGCACATGCGCTGGCTAATTTCTTAATTT	1261
Db	4556	AOCCECCAAATTAATTAACCAACAGTATACGCCACCAATACCTAATCTAATTTCTTAATTT	4497
QY	1262	TTTGTAGATAGGATCTCACTAATTTGTCCAGGCTGGTCTTTGAATTTCTGGGCTCAGGT	1321
Db	4496	TTTATATAAAAATTAATATCTCACTATTTATTCAAACTAATCTTAAATTCCTAAATCTCAAT	4437
QY	1322	GAGCTCCCACTGGGCGCTCCCAAAAGTATGGGATTAAGGATAGAGCAAGTCCCGTG	1381
Db	4436	AAACTCCCACTTAACCTCCCAAAATCTAAATTAACCAATTAACCAAAATCCCTCA	4377
QY	1382	CCCATATGAGATTTTCTGTCTCTGATGCCATGACAGCTAGTATCAAGCACTTGGCTGTG	1441
Db	4376	CCCATATTAATTAATTTCTATCTCTAATCCCAATCAACATTAATATCAAAAATTTAATCTA	4317
QY	1442	ACTCTGAGAGCACTGCAATGCTTTCTTGAAGCTGTGAATTCAGTGTAAAGCTCAAGGC	1501
Db	4316	ACTTAATAAAACCTACATATCTTTTAATCACTAAACTCAATCTAAAACTCATAAAC	4257
QY	1502	AGCCTTGAAACCCAAACCAAAAGTCTTAAGTTTATATCATCTGTATCAATGTGAATTTAT	1561
Db	4256	AACTCTTAACCCCAACCAAAATTTCTATTAATTTATATCCCAATCATTAATTTAT	4197
QY	1562	AGAAATTAACAATGATTTAAAGACACTACCCCTCAACTGAGCAAACTTAAGTAATTTT	1621
Db	4136	AAAAATTAACATTAATTTAAACACCTACCCCAACCTTAACCAAACTTAATTAATTTT	4137
QY	1622	TTAAAGTTTGACTGTTTTAAATCACTCTTGGAGAAAAAGAAAAATTAATCAATAT	1681
Db	4136	TTAAATTTAAGCTATTTTAAATCACTTATTAATAAAAAATTAATTAACAAATAT	4077
QY	1682	TAAAGGTGAATACAGGCTACTATACCTTTGTCTCAGAAATTAAGAGTCTGTCTTTTC	1741
Db	4076	TAAACATTAATTAACAACTACTATACCTTTATCTCCAAATTTAACAAATTTCTTTTC	4017
QY	1742	TTGCTTATGATGCTGAGGAGGAGGACACTGTGATTTGATGCTGTATATGAATGAATGCT	1801
Db	4016	TTACTTTAATATCTAATAATCAAAAAACACTTAAATTAATTAATTAATTAATTAATTAAT	3957
QY	1802	ATGTGTATTTTTTCTCAGCTGCTATGATTTGATTAATGCTAATTAATGAATGAATGCT	1861
Db	3956	ATATATATTTTTTCTCAGCTACTATTAATTAATTAATTAATTAATTAATTAATTAAT	3897
QY	1862	GATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCTGGAA	1921
Db	3896	AATAAAAAACACACAAACCAATTAATTCCTCAATCAATTTCTCTCAAAAACTTAATA	3837
QY	1922	TGTGCAATTAACAGTGGGAGATGATACCGGACAGACCCATGAAGAAAGATCAACAATT	1981
Db	3836	TATACATTAATCAATTAATAATAATATACCTTAACCAACCATTAATAATAATAACAATTT	3777
QY	1982	CCACCAGGAGACCCATTTTTCTTAATTTCAATTTGAATGAGCTCTAATGTCCCTCTT	2041
Db	3776	CCACCAGAAAAACCCATTTTTCTTAATTTCAATTTGAATTAATTAATTAATTAATCTCTT	3717
QY	2042	TCAATTCGTGCTTCTACCAAGTTTATACAGTTTTCGTGGTTCAATGTAATCAATAC	2101
Db	3716	TCAATTCCTACTCTTAACCAATTTTACAATTTTCTAATTTCAAAATTAATACTCAATAC	3657
QY	2102	ACTCATTTTTTCCATACCAAAACCCCAAGTACCCCAATGATGCCCATTTCCGATATAG	2161
Db	3656	ACTCATTTTTTCCATACCAAAACCCCAATTAACCAATTAATTCCTCATCTTGGATATATA	3597
QY	2162	TAAAGAGGCTGTGATTAAGGGCTGTGTCAAGGACGCAAGCTGAGAGGCTTGAAGCTG	2221
Db	3596	TAAAAAAAATCTAATTAATAAACTTATCAAAAACGCAACTAAAAACGCTAATAACTA	3537
QY	2222	GCTCATTTCAATCTATTTCTCACTGAATTTGACTTACCAAGACCCCAATGTGGGCT	2281

Db	3536	ACTGCATTTCGATCTCTATTCTGCTTAACCTTTAATCTAACCCAAATCATATTAAC	3477
Qy	2282	CTCGAATTCGATCAATTAATTTCTATTAGAAGCAAAAACAATTCGCCGATGGCCCCG	2341
Db	3476	CTCAATTTGATCAATTAATTTCTATTAAAAACAATAATTCGCCGATTAACCCCAA	3417
Qy	2342	TTATTAGAATTCCTCGATTACCTTGAGAAAAGCCCATCGGCTGTAATTCAGATCT	2401
Db	3416	TTATTAAACATTTCTCAAAATTTACCTTAATAAATAACCATGACCTATATATTCAGATCT	3357
Qy	2402	TCACCCCTTGTCCTCTCCCTAGAAAAGAAAGTCAGTTGATGACCCCTCGAGAACTA	2461
Db	3356	TCACCCCTTATCCCTCTCTCCCTAATAAATAAATAATCAATTAAATACCTTAATAAATA	3297
Qy	2462	GTGATGAGCTTAACCTGTCCTTCGATGAACCTGCTGCTTATCTGTTTCTATTTTCCTCT	2521
Db	3296	ATATCATTACTTAATCTATCTCTCCATACCTCTCAATCTATCTATTTCTATTTTCCTCT	3237
Qy	2522	TTCCACCGGAATCTATATATCTCAAGAAAAGAGGCACTGGCTTAAGGGCTCCGGCCCTAA	2581
Db	3236	TTCCACCGGAATCTATATATCTCAAAAAACAACACTTAACCTTAAATCCTTAACCTTA	3177
Qy	2582	GAATATCAAGTCCAGTGAAGAAATCCCATGTAAGTCAACCCCTCCGCTTACCCCTTGTGA	2641
Db	3176	AAATATTCATTCATTAATAAATCCCATTAATCAACCCCTCTCACTTAACCCCTTTATTA	3117
Qy	2642	TGAGAAAGCTCCAGGGGTTTGCTTTTTCATGATGATTAACAGGCTCACTCAGCATCACAG	2701
Db	3116	TAAATAAACTCCCAAAATTTACTTTTAACTATTACCAACCTAATCAACATCACAA	3057
Qy	2702	GGGCAAGAAAAGAAAGTAACCTTAATATGCTGCTTAATATGTAATTAATGTAATAG	2761
Db	3056	AAACAAAAAATAAAAAATTAACCTTAATATCACTTAATATTAATTAATTAATTAATTA	2997
Qy	2762	TTAATTACTGATTTGTATACATGTGTAAACAGAAATGTGTAATTTTTCACAGCTGCTG	2821
Db	2996	TTAATTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2937
Qy	2822	TGATTTGATTTATGCACTTTGGAATTAAGAAATGCTGTTAAGACACAGACGCAAGTTCT	2881
Db	2936	TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2877
Qy	2882	CAAGTCCGTAACAATTTTTCAAAAGTTAAATTTAAATATCACTAATTTGAATCTATGCTG	2941
Db	2876	CAATTCGTAACAATTTTTCAAAATTTAAATTTAAATATCACTAATTTGAATCTATTA	2817
Qy	2942	ACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATATTAATCTATGT	3001
Db	2816	ACAAAAAATTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2757
Qy	3002	TAGAGATTTTGAACAATTAATTAATTTTCTCAAGGTTCAATTTCCCATTAACCTTAA	3061
Db	2756	TAAATAATTTTAAACAATTAATTAATTTCTCAAAATTTGCAATTTCCCATTAACCTTAA	2697
Qy	3062	TGAATGTCATCACTATATGGGCCCCGTGAGAGACTAATTAATCTGTAATTTGTAATATCA	3121
Db	2696	TAAATTAATCACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2637
Qy	3122	TTGTTATTAATTAATTAATTAATTTTGTGTTTAATGTAAGATTTTAAAGATATATGT	3181
Db	2636	TTAATTAATTAATTAATTAATTAATTTTACTTTAAATTAATTAATTAATTAATTAAT	2577
Qy	3182	AAACTGTAAACATTAATAATGCAAAATGCCCCGTAAGAGACAGTATGATTAATATATTT	3241
Db	2576	AAACTATTAATAATTAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTA	2517
Qy	3242	ATATTTGTTATCATTAATTAATGCTGTTTTCCTGTTGTAATTTTCTTCTTAAATGCTT	3301
Db	2516	ATATTAATTAATCATTAATTAATTAATTTTTCCTATTTTAATTTTCTTCTTAAATACTT	2457
Qy	3302	ACAGAAATCTGTAATCCCATTTCTTACACACACCCCAACAATTTGCTTCTTTTCCCA	3361

Db	1750	GAGGGTTTTTATTTAGTTTAAAGGAAGATTAAAGAAATGAAATATTTTATGATATATTAAGT	1809
QY	361	TACAAACACACACAGCAGGTTCACGAAAAAGGCTCAGCTGTGGAAACAGGTCACCCCAAC	420
Db	1810	TATTAATATTTATATAGTAGGTATTAAGAAAAAGGTTTACGGTGGAAATTAGGTTATTTTTAT	1865
QY	421	TCAGCAGACACAGTCATATTAATCAAGGACCAACAGAGGACAGAGAACCCCTCCCA	480
Db	1870	TTAGTAGATTTAGTTTATATTAATTAAGATTAATAGAGATAGAGAAATTTTTTTTTTA	1929
QY	481	CTCTGCCCAATGTCAGATTGATAGTGAGCCCTTCCTCAGATCTCTCCACCAATCTTAGA	540
Db	1930	TTTTTGTATTATAGTTTAAAGTTGATGAGTGTATTTTTTTTAAATTTTTGTATATTAATTAGA	1989
QY	541	AAGGACACCTGAAAGAAAGAACTGAAATTTTAGCTGACGCAATTAAGAGATGATTA	600
Db	1990	AAGGAATATTTGAAAGAAATTTGAATTTAATTTATATGATATTAAGAGATGATTA	2049
QY	601	ACCTAAATCAATGTTCAATGATGAAATGAATCAAGAGATTTAAACCACTTGAAGTAA	660
Db	2050	ATTTAAATATATGTTTAAATGATGAAATTAAGAGAAATTTAAATTTTGTGATTA	2109
QY	661	TGATGCAATCTTTTCTCTGCTATCCAGCAGATGAGAGCTGTGACAGACACATATA	720
Db	2110	TGATGCAATTTTTTTTTTTGTATTTAGTAGATGAGAAAGTTGATATAGATTAATA	2169
QY	721	GTTTGAAGACTAAAGAAATTCATGCAATTCCTGCTGAGTTGTATTTGATATTTTA	780
Db	2170	GTTTGAAGATTAAGAAATTTATGATATTTTATTTGATGATGATTTGATGATTTTA	2229
QY	781	GTTGACCTCATTTGTATTAATCTTGACACAGGGGCAATCCAAATGTCACAGAGATAG	840
Db	2230	GTTGATTTTATTTTGTAAATTTGTATTAAGGGATTTATATTTGT--ATAGAGATAG	2286
QY	841	TTAAACAGTGTAAATGCTGCATGAGAGAGATGGGATTTTATCTTTCGTTTTGTCT	900
Db	2287	TTAA-TAGGTATTAATGTTGATAGAGAGATGGGATTTTATCTTTCGTTTTGTCT	2345
QY	901	CTTCTTCTTATTTGTTCTTATCTTATTAAGATTAACCTATCGTTTCCAAATGTA	960
Db	2346	TTTTTTTTTTATGTTTATTTATTTAACGATTAATTTATCGTTTT--TAAATAGTAA	2404
QY	961	GGCATTTTGAAGCCTAATTCAAACCTCTCAGTATTTGTATTAAGTATTCACCTG	1020
Db	2405	GGTATATTTGAAGTTAAATTTAAATTTTATTTATTTGTATTTAAGATTAATTAATTTG	2464
QY	1021	ATTGAGCTGGGATAGACAGGTGAAACCAATACAGGTTTTTAAATTTTAAATTTTAA	1080
Db	2465	ATTGAGATGGGATAGATAGGTGAAATTAATTAATTTAGTTTTTAAATTTTAAATTT	2524
QY	1081	ATTATTTATTTATTTATTTTGTGAGATGAGTCTGCTGTCCAGGCTGAGTGCAG	1140
Db	2525	ATTATTTATTTATTTATTTTGTGAGATGAGTCTGCTGTCCAGGCTGAGTGCAG	2584
QY	1141	CGGCGTATACAGTTCACTGACGCTCAACCTTCTAGGCTCAAGGATTTCTCCACCTC	1200
Db	2585	CGGCGTATATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	2644
QY	1201	AGCCCCCAAGTATGGGACCAACAGATAGGCGCAACAGCCGCGCTAATTTCTAAT	1266
Db	2645	AGTTTTTAAAGTATGGGATTAACAGATAGGCGTTATTTATTTATTTATTTATTT	2704
QY	1261	TTTTTGAAGATAGGATCTCACTATTTATTTGTCAGGCTGTCTGAAATTCCTGGGCTCAG	1320
Db	2705	TTTTTGAAGATAGGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	2764
QY	1321	TGAGCTTCCACTGGGCTCCCAAGTACTGGGATTAACGACATGACCAAGTCCCT	1380
Db	2765	TGAGTTTTTAAATTTGGGTTTTTAAAGTATTTGGGATTTATGATTAAGGTTTTTT	2824
QY	1381	GCCATATAGATTTTCTGCTCTGATCCCATGACGCTAGTAATCAAGGACTTGGCTGCT	1440
Db	2825	GTTTATTAAGATTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTT	2884

1441 GACTCTGGAGGACCTGATGCTTTCTGAGCTGTGAACCTTCAGTCTTAAGCTCATAGG 1500
2885 GATTTTGGAGGATTTGTATGTTTTTTTGGAGTTGTGAATTTTAGTGTAAAGATTATAGG 2944
1501 CAGCCCTGAAACCCAAACCAAGGTTCTATAGGTTTATCATCTGATCATGTGTATTTA 1560
2945 TAGTTTGAATAATTTAAATTTAAAGGTTTATAGGTTTATTTGATTAATGTGTATTTA 3004
1561 TAGAATAACACATGAATTTAAAGACATACCTCAACTGAGCAAACTTAAGTATTTT 1620
3005 TAGAATAATATATATGAATTTAAAGATTTATTTTAAATGAGTAAATTTTAAGTATTTT 3064
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3065 TTTAAAGTTTGAATTTGTTTTTAAATTTATTTTGGAGAAAAGAAAATTAATTAATTA 3124
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3125 TTTAAGGATATATAGGTTATATATATTTTGTGTTTTTGAATTTAGTGTGTTTTTTT 3184
1741 CTGCTTAGATGCTGAAGTGAAGACACCTGCTGATGCTGATGCTGATGCTGATGCTG 1800
3185 TTTGTTTATGATGTTGAAGTGTGAAGATATTTTGTGATTTGACGTGTATGATTTA 3244
1801 AATGTATTTTTTTTTCTCAGCTGCTATGATTTGATTTATGCTATTTATGATTAAGATGC 1860
3245 AATGTATTTTTTTTTTATGTTTATGATTTGATTTGATTTATGATTTATGATTAAGATGC 3304
1861 TGATGAGGACACACAAACCAATTTGCTCTGATGCTATTTCTCTCTCAAAAGCTGGA 1920
3305 TGATGAGGATATATTAATTTATTTGTTTTTATGTTTTTATTTTTTTTTTAAAGTTTGA 3364
1921 ATGTCATTTGATGCTGAGGAGATGATGACCTGAGACAGACCATGAAAGAGATCAACAAT 1980
3365 ATGTTTATTTATGATGAGGAGATGATTTGATTTGATTTATGAAAGATTTATTAAGT 3424
1981 TCCACCAAGGAGACCTATTTTTCTTAATTTCAATTTGAATGCTTCTAATTTGCTCTCT 2040
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2041 TTTATTTCTGCTCTCTCAACAGTTTACAGCTTTTCTGCTTCAATTTGAATGCTCACTA 2100
3485 TTTATTTTGTGTTTTTATAGTTTATAGTTTTTGTGTTTTTAAATGGAATTTATATA 3544
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3545 TATTTTATTTTTTTTATTTATTTAATTTTAAGTATTTAATGTTTTTATTTTGGATATA 3604
2161 GTAAAGAGGCTCTGATTAAGGCTTTGCAAGGACGCACTGAGAGGCTTAGACT 2220
3605 GTAAAGAGGCTTTGATTAAGGCTTTGTTAAGGATGATGAGAGGCTTAGACT 3664
2221 GGCCTCATTTTCATCTATTTCTCACTGACTTTGACTACCAAGAACCCCAATGTGGG 2280
3665 GCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAAATTTAATGTGGG 3724
2281 CCGTATTTGATGAATTAATTTCTAATTAAGACAAAACATTTCCCGCATTTGGCCCA 2340
3725 TTTTATGATTTCAATTAATTTATTTAAGAGTAAATTTTATTTTATTTTATTTT 3784
2341 GTTATTAAGCATTTCTCAATTTACCTTGAGAAATGCCATGCGCTGTATATTTCAATC 2400
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3845 TTTATTTTGTGTTTTTTTTTGAAGAGAAAGTATGATGATGTTTTTTTGAAGAAAT 3904
2461 AGTGAATGCTTAACGCTTCATGATCGCTGAGCTTATGCTTTATTTTCTCTCT 2520
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4085 ATGAGAAAGTTTAAAGGCTTTGTTTTTGTATGTTATTAAGGTTAATTTAGTATTTA 4144
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4145 GGGGTAAGAAAAGAAATGATTTTAAATTAATGTTTATTAATTTATTTATTTATTTA 4204
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2821 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2880
4265 GTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 4324
2881 TCAATGCTGAGCAATTTTCAAAAGTAAATTTAAATTTCACTACATTTGAATCTAGT 2940
4325 TTAAGTTGATGATTAATTTTAAAGTAAATTTAAATTTAAATTTAAATTTAAATTTAGT 4384
2941 GACAGAGAAATGACATGATTAAGACATAAGATCTAGCCCAATTTTATTTATTTACTTG 3000
4385 GATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4444
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4505 ATGAATGCTTATTAATTTAAGGCTTTGAGAGATTAATTTAATTTAATTTAATTTAAT 4564
3121 ATTTTATTTATTTATTAATTTTATTTTGTCTTTTAAATGATTAAGATTTTAAAGTATAG 3180
4565 ATTTTATTTATTTATTTATTTATTTTGTCTTTTAAATGATTAAGATTTTAAAGTATAG 4624
3181 TAACTGTAAACATTAATGCAAAATGCCGTAAAGACAGTATTAATTAATTAATTAAT 3240
4625 TAAATTTGAAATTAATTAATGCAAAATGCCGTAAAGACAGTATTAATTAATTAATTA 4684
3241 TATATTTGATTAATTTAAGCTGTTTTTCTGTTGTATTTCTCTTAAATAGCT 3300
4685 TATATTTGATTAATTTAATTTAATTTTGTGTTTTTGTGTTTTTAAATGAT 4744
3301 TACAGAAATCTGATCCCAATCTTCAACACCAACCAATTTCTGCTCTTTCC 3360
4745 TTTAAGAAATGATTTTATTTTATTTTATTTATTTTAAATTTTGTGTTTTTTT 4804
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4805 ATGCGGTTATGTTAATTTTGAAGTTTATGTTTTTTTTTTTTTAAATTTTGTG 4864
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4865 TATTTTGTATGTTTTTGAATTTATGTTAAAGATTTTATGTTTATTAATG 4924
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4925 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4984
3540 TCAATTTGATGATGATTTTCTCTCTATCAAGGAGATGTA 3586
4985 TTAATGAGGATTTATTTTTTTTTTATTAATGAGGAGATGTA 5031

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; Schweickart, Vicky L.
; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
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; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
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; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 362..1426
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-28 polynucleotide and amino acid
; sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
; US-10-106-623-3
; Query Match 9.6%; Score 344.2; DB 5; Length 1915;
; Best Local Similarity 98.9%; Pred. No. 4,6e-67;
; Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 3227 ATAAATATGATTATATATGTTATATCTAGAGCTGTTTCTGTTGTAATTC 3286
DB 1 ATAATATGATTATATATGTTATATCTAGAGCTGTTTCTGTTGTAATTC 60
QY 3287 TTCCTTAATGCTTACAGAAATCTGTATCCCATCTTACACACACCCCAACAATT 3346
DB 61 TTCCTTAATGCTTACAGAAATCTGTATCCCATCTTACACACACCCCAACAATT 120
QY 3347 CTGCTCTTTCCCATGCC-GGTCATGCTACTTAAGCTTCAAGCTCTTCTCTCTC 3405
DB 121 CTGCTCTTTCCCATGCCGGGTCATGCTAACTTGAAGCTTCAAGCTCTTCTCTCTC 180
QY 3406 AATCTCTTCCGACCTCTGATAGCCTTTGAATTCAGTTAAAGATCCCAAGC 3465
DB 181 AATCTCTTCCGACCTCTGATAGCCTTTGAATTCAGTTAAAGATCCCAAGC 240

QY 3466 TCGTATCACATGCGCATCTTGTGAGTACATGATAATCACTGGTGTATTACGA 3525
DB 241 TCGTATCACATGCGCATCTTGTGAGTACATGATAATCACTGGTGTATTACGA 300
QY 3526 AGAATGATTATGCTTCAATTTGGGATTTGATTTTCTTTCTATCACAGGAGAGTA 3585
DB 301 AGAATGATTATGCTTCAATTTGGGATTTGATTTTCTTTCTATCACAGGAGAGTA 360
QY 3586 A 3586
DB 361 A 361
RESULT 8
US-10-772-037-3
; Sequence 3, Application US/10772037
; Publication No. US20040230037A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Schweickart, Vicky L.
; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/772,037
; FILING DATE: 04-Feb-2004
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 362..1426
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-28 polynucleotide and amino acid
; sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
; US-10-772-037-3
; Query Match 9.6%; Score 344.2; DB 8; Length 1915;
; Best Local Similarity 98.9%; Pred. No. 4,6e-67;
; Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 3227 ATAAATATGATTATATATGTTATATCTAGAGCTGTTTCTGTTGTAATTC 3286
DB 1 ATAATATGATTATATATGTTATATCTAGAGCTGTTTCTGTTGTAATTC 60

QY 3287 TTCCTTAATGCTTACAGAAATCTGTATCCCATCTTCACACACCCCAACATTT 3346
DB 61 TTCCTTAATGCTTACAGAAATCTGTATCCCATCTTCACACACCCCAACATTT 120
QY 3347 CTGCTCTCTTCCCATGCGC-GGTCAATGCTTACAGAAAGCTTCTCTCTCTC 3405
DB 121 CTGCTCTCTTCCCATGCGCGGTCAATGCTTACAGAAAGCTTCTCTCTCTC 180
QY 3406 AATCCCTTCCTGGGACCTGTATGCTTCTTGAATTCATGTTAAAGATCCCTAGGC 3465
DB 181 AATCCCTTCCTGGGACCTGTATGCTTCTTGAATTCATGTTAAAGATCCCTAGGC 240
QY 3466 TCTCATCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 3525
DB 241 TCTCATCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 300
QY 3526 AGAATGATTAATGCTTCAATGTCATGTCATGTCATGTCATGTCATGTCATGTC 3585
DB 301 AGAATGATTAATGCTTCAATGTCATGTCATGTCATGTCATGTCATGTCATGTC 360
QY 3586 A 3586
DB 361 A 361

RESULT 9

US-09-925-065A-727856
Sequence 727856, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Manq, David G.
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 727856
LENGTH: 3771
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-727856

Query Match Best Local Similarity 72.2%; Pred. No. 1,1e-37; Length 3771;

Matches 280; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1042 GAAACCATATCAGGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1101
DB 1961 GAAACCATATTTTAACTGTACCTTTTCTATGTTTGGCTATTTTGGCTTTGTTT 2020
QY 1102 TTGAGTAGAGTGTGCTGTGCGCCAGGCTGAGTGTGAGGCGGTATCATTTACG 1161
DB 2021 TTGAGTAGAGTGTGCTGTGTTGAACAGGCTGAGTGTGAGGCGCAATCTGCTCACTG 2080
QY 1162 CAGCTCAACCTTCTAGAGCTCAAGGATTTCCACCTCAGCCCAAGTAGTTGGAGC 1221
DB 2081 CAGCTCAACCTTCTAGAGCTCAAGGATTTCTGCTCTGCTGCTCCCAAGTAGTTGGAGC 2140
QY 1222 CAGCTCAACCTTCTAGAGCTCAAGGATTTCTGCTCTGCTGCTCCCAAGTAGTTGGAGC 1281

DB 2141 TACAGGACCTGCGACCATGCTTACCTAATTTTGTATTTTGTAGAGACAGGCTTCA 2200
QY 1282 CTATATGTCAGAGCTGCTTGAATTCCTGGGCTCAGGTGAGCTCCACCTGGGCTTC 1341
DB 2201 CCAATGTGGCCAGGCTGCTTGAATTCCTGAGCTTCAAGTATTCGGCCACCTTGGCTTC 2260
QY 1342 CCAAGTACTGGATTTACAGGATGAGCCAGAGTCCCTGCTCCATATGATTTCTGTC 1401
DB 2261 CCAAGTACTGGATTTACAGGATGAGCCAGAGTCCCTGCTCCATATGATTTCTGTC 2320
QY 1402 TCTGATCCCATGCTAGTATCAAGG 1429
DB 2321 TTAATCCCATCTTAAAGAAAGCTAGG 2348

RESULT 10

US-09-925-065A-804603
Sequence 804603, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Manq, David G.
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 804603
LENGTH: 606
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-804603

Query Match Best Local Similarity 5.9%; Score 212.4; DB 4; Length 606;

Matches 273; Conservative 1; Mismatches 102; Indels 0; Gaps 0;

QY 1023 TGAGCTGGGTAGACAGGTGAACCATATCAGGTTTAAATTTTAAATTTTAAATTTAT 1082
DB 103 TGAGGAAGAGTCTAAGGTCATATTTCTTTTAAATTTTAAATTTTAAATTTAT 162
QY 1083 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1142
DB 163 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 222
QY 1143 GGTATGACAGTTCATGCTCAGCTCAACCTTCTAGGCTCAAGGATTTCTCCACCTCAG 1202
DB 223 GGTATGACAGTTCATGCTCAGCTCAGCTCCTGCTGTTAAGACATTTCTGCTCTCAG 282
QY 1203 CCCCCCAAGTATGAGGACACAGTATGCGCACCAAGCTGAGTAAATTTCTTATTTT 1262
DB 283 CCAATGATCTAGCTCAGCTCAGCTCAGCTCCTGCTGTTAAGACATTTCTGCTCTCAG 342
QY 1263 TTGTAAGATAGATTTCTATATTTTCAAGCTGCTGCTTGAATTTCTGAGCTCAGG 1322
DB 343 TTGTAAGATAGATTTCTATATTTTCAAGCTGCTGCTTGAATTTCTGAGCTCAGG 402
QY 1323 AGCTCCCACTGGGCTCCCAAGTATGAGGATTTACAGGATTAAGGATTAAGGATCCCTGC 1382
DB 403 TTCCACCACTCTGGCTCCCAAGTATGAGGATTTACAGGATTAAGGATTAAGGATCCCTGC 462
QY 1383 CCAATGATATTTTCT 1398

QY 1109 GGAGTCTGCTGTCGCCAGGCTGAGTGCACGGCGTGATCAAGTTCACTGCAGCCTC 1168
DB 2852 CGTTTGCTCTGTCCGCCAGGCTGAGTGCATGCGGTGATCTCAGCTCACTTCAACCTTC 2793
QY 1169 AACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGACCAACGT 1228
DB 2792 CACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGATTTACAGAT 2733
QY 1229 ATGCCCAACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATCTCATATAT 1288
DB 2732 GCATGCCACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATGCGGTTTACCATGTT 2673
QY 1289 GTCCAGGCTGCTCTTGAATTTCTGCGCTGAGTGCAGCTGCCAAGCTTCCCAAGT 1348
DB 2672 GGCACAGGCTGCTCTGAACTCCCGGCCAGATGATCCGCGCTCAGCCTCCCAAGT 2613
QY 1349 ACTGGGATTTACAGGATGAGCCCAAGTCCCGCTCCCATATGAGATTTTCTGCTCGATC 1408
DB 2612 GTTGGGATTTACAGGATGAGCCATGCTGCTGCGCTTCTAGACTGTTACTTAAATGGGTC 2553
QY 1409 CCATGAGCTAGTAATCAAGACTTGGCTGCTGACTCTG 1447
DB 2552 TTTTGAACATATATTTTAGGCAACTTTTATTAACCTTG 2514

RESULT 14

US-10-087-192-946
; Sequence 946, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 946
; LENGTH: 54701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(54701)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-946

Query Match 5.9%; Score 211.8; DB 5; Length 54701;
Best Local Similarity 70.7%; Pred. No. 2.7e-36;
Matches 282; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1049 AATACAGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1108
DB 37898 ATTTGTTGTTTAACTAAATATGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 37957
QY 1109 GGAGTCTGCTGTCGCCAGGCTGAGTGCAGCGGCTGATCAAGTTCACTGCAGCCTC 1168
DB 37958 CGTTTGCTCTGTCCGCCAGGCTGAGTGCATGCGGTGATCTCAGCTCACTTCAACCTTC 38017
QY 1169 AACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGACCAACGT 1228
DB 38018 CACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGATTTACAGAT 38077
QY 1229 ATGCCCAACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATCTCATATAT 1288
DB 38078 GCATGCCACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATGCGGTTTACCATGTT 38137

QY 1289 GTCCAGGCTGCTCTTGAATTTCTGCGCTGAGTGCAGCTGCCAAGCTTCCCAAGT 1348
DB 38138 GGCACAGGCTGCTCTGAACTCCCGGCCAGATGATCCGCGCTCAGCCTCCCAAGT 38197
QY 1349 ACTGGGATTTACAGGATGAGCCCAAGTCCCGCTCCCATATGAGATTTTCTGCTCGATC 1408
DB 38198 GTTGGGATTTACAGGATGAGCCATGCTGCTGCGCTTCTAGACTGTTACTTAAATGGGTC 38257
QY 1409 CCATGAGCTAGTAATCAAGACTTGGCTGCTGACTCTG 1447
DB 38258 TTTTGAACATATATTTTAGGCAACTTTTATTAACCTTG 38296

RESULT 15

US-10-719-993-6833
; Sequence 6833, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6833
; LENGTH: 60316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6833

Query Match 5.9%; Score 211.8; DB 8; Length 60316;
Best Local Similarity 70.7%; Pred. No. 2.8e-36;
Matches 282; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1049 AATACAGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1108
DB 46727 ATTTGTTGTTTAACTAAATATGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 46786
QY 1109 GGAGTCTGCTGTCGCCAGGCTGAGTGCAGCGGCTGATCAAGTTCACTGCAGCCTC 1168
DB 46787 CGTTTGCTCTGTCCGCCAGGCTGAGTGCATGCGGTGATCTCAGCTCACTTCAACCTTC 46846
QY 1169 AACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGACCAACGT 1228
DB 46847 CACCTTCAAGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTGTGGGATTTACAGAT 46906
QY 1229 ATGCCCAACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATCTCATATAT 1288
DB 46907 GCATGCCACATGCTGCTGCTAATTTCTTATTTTTTTGTAGATAGATGCGGTTTACCATGTT 46966
QY 1289 GTCCAGGCTGCTCTTGAATTTCTGCGCTGAGTGCAGCTGCCAAGCTTCCCAAGT 1348
DB 46967 GGCACAGGCTGCTCTGAACTCCCGGCCAGATGATCCGCGCTCAGCCTCCCAAGT 47026
QY 1349 ACTGGGATTTACAGGATGAGCCCAAGTCCCGCTCCCATATGAGATTTTCTGCTCGATC 1408
DB 47027 GTTGGGATTTACAGGATGAGCCATGCTGCTGCGCTTCTAGACTGTTACTTAAATGGGTC 47086
QY 1409 CCATGAGCTAGTAATCAAGACTTGGCTGCTGACTCTG 1447
DB 47087 TTTTGAACATATATTTTAGGCAACTTTTATTAACCTTG 47125

Search completed: January 7, 2006, 20:31:28
Job time : 2608.82 secs

ORIGIN

Query Match 7.5%; Score 267.6; DB 9; Length 549;
Best Local Similarity 84.4%; Pred. No. 1e-31;
Matches 335; Conservative 0; Mismatches 57; Indels 5; Gaps 3;

QY 924 ATTATGATTAACCTTATCGTTTCCCAAAATGTAAAGGCCATT-TTGAAGCCTTAATTC 982
DB 396 ATATAGAAAGGATATCATGATATACAAATGTATACAGAGCCCATGTATGAGAGCTTAATTC 337
QY 993 AAACCTCTTCA--CTATTTTGTATCTAAGTATTCACCTTATGAGACCTGGGTAGACAG 1040
DB 336 GATCATCTCCCACTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 277
QY 1041 TGAATACCATATCAGGTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1100
DB 276 TGAATACCATATCAGGTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 219
QY 1101 TTTGAGATGAGCTTGGCTGTGCGCCAGGCTGAGTGAAGCGGCTGATCAAGTTCACT 1160
DB 218 TTAGAGATGAGCTTGGCTGTGCGCCAGGCTGAGTGAAGCGGCTGATCAAGTTCACT 159
QY 1161 GAGGCTCAACCTTCTAAGGCTAAGGGAATTCCTCCACCTCAGCCGCCCAAGTATGGA 1220
DB 158 GAGGCTCAACCTTCTAAGGCTAAGGGAATTCCTCCACCTCAGCCGCCCAAGTATGGA 99
QY 1221 CCACAGTATGAGCGCCACATGCGCTGCTAATTTCTAATTTTCTTATTTTGTAGAGATGATCTC 1280
DB 98 CCACAGTATGAGCGCCACATGCGCTGCTAATTTCTAATTTTCTTATTTTGTAGAGATGATCTC 39
QY 1281 ACTATATGTCCAGGCTGTCTTGAATTCCTGGGCTC 1317
DB 38 ACTATATGTCCAGGCTGTCTTGAATTCCTGGGCTC 2

RESULT 2 BE677425 453 bp mRNA linear EST 08-SEP-2000
LOCUS BE677425
DEFINITION 7d8b05.x1 lupski dorsal root ganglion Homo sapiens cDNA clone
IMAGE:3279633.3, similar to contains Alu repetitive
element;contains element MER35 repetitive element; mRNA sequence.

ACCESSION BE677425
VERSION BE677425.1 GI:10037894
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Carcharia;
Hominidae; Homo.
1 (bases 1 to 453)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James Lupski
CDNA Library Preparation: Lupski Laboratory
CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E.B. Consortium/LNL at:
info@image.lnl.gov
Seq primer: -40UP from Glibco
High quality sequence stop: 406.
Location/Qualifiers
1. 453

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3279633"
/sex="male"
/tissue_type="dorsal root ganglia"

ORIGIN

Query Match 5.9%; Score 210; DB 2; Length 453;
Best Local Similarity 76.3%; Pred. No. 9.9e-23;
Matches 258; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1064 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1123
DB 3 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 62
QY 1124 CCCAGGCTGAGATGAGCGGCTGATCAAGTTCACTGAGGCTCAAGCTTCTAGGCTCA 1183
DB 63 CCCAGGCTGAGATGAGCGGCTGATCAAGTTCACTGAGGCTCAAGCTTCTAGGCTCA 122
QY 1184 AGGAGATCTCCACCTCAGCCGCCCAAGTATGAGGACACAGTATGCGCCAGATGCC 1243
DB 123 AGGAGATCTCCACCTCAGCCGCCCAAGTATGAGGATGACAGGATGACAGATGAC 182
QY 1244 TGGCTAATTTCTTATTTTGTGAGAGATGAGATCTCAATATTTGTCAGGCTGCTT 1303
DB 183 TGGCTAATTTCTTATTTTGTGAGAGATGAGATCTCAATATTTGTCAGGCTGCTT 242
QY 1304 GAATTCCTGGGCTCAGTGAAGCTCCACCTGCGGCTCCCAAGTATGAGGATACAGGC 1363
DB 243 CAATTCCTGGGCTCAGTGAAGCTCCACCTGCGGCTCCCAAGTATGAGGATACAGGC 302
QY 1364 ATGAGCCAAAGTCCCTGCGCCATATGAGATTTTCTGTC 1401
DB 303 ATGAGCCAAAGTCCCTGCGCCATATGAGATTTTCTATTC 340

RESULT 3 AG114100/c
LOCUS AG114100 700 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-120022.R, genomic survey sequence.
ACCESSION AG114100
VERSION AG114100.1 GI:16734619
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Carcharia;
Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 700)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsukuba-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbese@sc.riken.go.jp, URL:http://hsp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

COMMENT
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_id="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCAAGGCTCCG-3' and
5'-GACTAGTCTTATGATGCGAGCGGCGCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

[illegible][illegible]

Db	1195	CACCTCAAGCCCGGCAAGTAAATTTGGAGAACCAAGTAATGGCACAAGTATGCCTGGCTAATTTC
Qy	1194	AATTTTCTCTCTTGTTTTTTTTTTTAGAGAGAGCTCT--GGCTGCCCCAGGCTGGA
Db	513	GTCGAGTGTGTGATCTCAGCTCATCGACCTCCACCTCCAGGTTCAAGTGAATTC
Qy	512	GTGCGAGCGCGGTGATCACAGTTCACTGACGCTCAACCTTTAGGCTCAAGGATTC
Db	1077	AATTTTCTCTCTTGTTTTTTTTTTTAGAGAGAGCTCT--GGCTGCCCCAGGCTGGA
Qy	1076	AATTTTCTCTCTTGTTTTTTTTTTTAGAGAGAGCTCT--GGCTGCCCCAGGCTGGA
Db	242	GCGAGGCTGGTCTTGACTCTTGACCTTAGATACTCCTGGCTTGGCTCTGAAGTG
Qy	241	TCCAGGCTGGTCTTGAAATTCCTGGGCTCAGGAGGCCGCCACCTGGGCTCCCAAAGTA
Db	182	CTCGGCACCAACACCAGCTAATTTTGTATTTAGTAGAGACGGGGTTTCCACATGTG
Qy	1290	CTGGGATTACAGGACATGAGCCAGAAGTCCCCTGCCCATATGAGATTTCTGTCTGATCC
Db	302	CTGAGATTACAGGACATGAGCTGTGTGTGCCCCAGCCTATTAAGTAATTTCTTACGAGCA
Qy	1410	CATGCACTAGTATTCAGAACT
Db	362	TACCAATCTCTTCATTCATTTGACT
RESULT_9	BZ772437/c	686 bp DNA linear GSS 13-MAR-2003
LOCUS	mcv36f03.g1	HFOSMID007 Homo sapiens genomic, genomic survey
DEFINITION	BZ772437	sequence.
ACCESSION	BZ772437	
VERSION	BZ772437.1	GI:28946121
KEYWORDS	GSS,	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheraia; Euarchontoglires; Primates; Catarrhini;	
	Homnidae; Homo.	
REFERENCE	1 (bases 1 to 686)	Cook,L., Delehaunty,K., Fewell,G., Fulton,L., Magrini,V.,
AUTHORS	Mardis,E., Miner,T., Nash,W., Williams,D. and Wilson,R.K.	
TITLE	Homo sapiens Fosmid End Reads	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Richard K. Wilson	
	Genome Sequencing Center	
	Washington University School of Medicine	
	Email: submissions@watson.wustl.edu	
	Plate: mcv36 row: f column: 03	
	Class: fosmid ends	
	High quality sequence start: 44	
	High quality sequence stop: 526.	
FEATURES	location/Qualifiers	
source	1..686	/organism="Homo sapiens"
		/mol_type="genomic DNA"
		/db_xref="taxon:9606"
		/clone_id="HFOSMID007"
		/note="Vector: pcc01fos; Site 1: Eco72I; Human whole
		genome fosmid library was prepared at Washington
		University Genome Sequencing Center. DNA was sheared for
		blunt-ended ligation into pcc01fos inducible vector. DNA
		was ordered from Coriell Cell Repository s DNA
		polymorphism discovery resource."
ORIGIN		
Query Match	5.7%; Score 205.6; DB 9; Length 686;	
Best Local Similarity	80.6%; Pred. No. 4,3e-22;	
Matches 253; Conservative	0; Mismatches 59; Indels 2; Gaps 1;	

Df		453	TACCTCAGCCCTCGATGACTGTGGAAATTACAGGCATCGCTACCATCTGGCTAATTTT	394
Oy		1255	TTAATTTTTTTTGTAAGATATAGATCTCACTATATTTTCAGAGCTGTCTTGAATTCCTGGG	1314
Df		393	TTCAATTTTGTGTAGACAGAGTTTGTGCCAATGTGTGCACAGCTGTCTCGAACCTCTGAC	334
Oy		1315	CTCAGGTGAGCTCTCCCACTGGGCTCCCAAAGTACTGGAGATTACAGGCATGAGCCAAGG	1374
Df		333	CTCAGGTGATTCGGCCCACTCTGGCTCCCAAACGTGTGGATTACAGGCATGAGCCACTG	274
Oy		1375	TC CCTGCCCCATAT 1388	
Df		273	TGCTCGAGCATTT 260	
RESULT 10				
BX485916				
LOCUS				
DEFINITION			501 bp mRNA linear EST 04-SEP-2003	
ACCSSION			DKFZp686E13249.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone	
VERSION			DKFZp686E13249.5, mRNA sequence.	
KEYWORDS			BX485916 BX485916.1 GI:31949114	
SOURCE			EST.	
ORGANISM			Homo sapiens (human)	
			Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
			Hominoidea; Homo.	
			1 (bases 1 to 501)	
REFERENCE			Ansoerge,W., Krieger,S., Regiert,T., Rittmeller,C., Schwager,B.,	
AUTHORS			Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and	
			Wiemann,S.	
			EST (Ansoerge,W., Krieger,S., Regiert,T., Rittmeller,C., et al.)	
TITLE			Unpublished (2003)	
JOURNAL			Contact: MIPS	
COMMENT			MIPS	
			IngoIsaetler Landstr.1, D-85764 Neuherberg, Germany	
			This is the 5' sequence of the clone insert	
			Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
			Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;	
			sequenced by EMBL (European Molecular Biology Laboratories),	
			Heidelberg/Germany) within the cDNA sequencing consortium of the	
			German Genome Project.	
			No sl sequence available.	
			This clone (DKFZp686E13249) is available at the RZPD in Berlin.	
			Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059	
			Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.	
FEATURES			location/Qualifiers	
SOURCE			1..501	
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			/db_xref="taxon:9606"	
			/clone="DKFZp686E13249"	
			/dev_stage="adult"	
			/lab_host="DH10B"	
			/clone_1lb="686 (synonym: hlcc3)"	
			/note="Vector: pTRIPlex2; Site_1: SfiIA; Site_2: SfiIB;	
			cDNA-collection"	
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Query Match		5.7%; Score 205.2; DB 5; Length 501;		
Best Local Similarity		76.7%; Pred.No.5.4e-22;		
Matches 264; Conservative		0; Mismatches 78; Indels 2; Gaps 1;		
Oy		1057	TTTTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTGAATGAGTCTG	1116
Df		9	TTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAATGAAGCTTT	68
Oy		1117	G--CTGTGCCCAGAGCTGAGTGCAGCGGCGCTGATCAAGTTCACTGCAAGCTTCAACCTT	1174
Df		69	GCTCTGTGTTCCCAAGCTGAGATGTCTGTGGATGATCGGGGCTCACTCAACTCTGCTT	128
Oy		1175	CTAGGCTCAAGGATTTCTCCACCTCAGCCCCCAAGTAAATGTGGAGCACACATATGGC	1234

Db 129 CTGGGTTCAAGATGATTCCTGCGCTCAGCTCCAGTAGCTGGAGATTACAGCATGTC 188
Qy 1235 CACCATGCTGGCTAATTTCTTAATTTTGTAGAGATAGATCTCACTAATTTGTCAG 1294
Db 189 CACCATGCTGGCTAATTTTGTATTTTATATAGAGACAGGTTTCACTATTTGGCCAG 248
Qy 1295 GCTGCTCTTGAATTCCTGGGCTCAGGTGAGCTCCCACTGGGCTCCCAAGTACTGGG 1354
Db 249 GCTGTTCTCAAACTCTGACCTCAAGTATCTGCCCACTGGGCTCCCAAAATGTTGGG 308
Qy 1355 ATTACAGGATGAGCCAAAGTCTCCCTGCCCATATGAGATTTCT 1398
Db 309 ATTACAGGCTGAGGACCTGCGCTGGGCTCCCTGTAGGCTTTT 352

RESULT 11
CN274852 533 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600044196 GRN_PRENEM Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN274852
ACCESSION CN274852.1 GI:47291266
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 533)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowicz, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 533 Std Error: 0.00.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEM"
/note="Oligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN
Query Match 5.7%; Score 204.8; DB 7; Length 533;
Best Local Similarity 73.9%; Pred. No. 6.1e-22;
Matches 260; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 1045 AACCATATCAGGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1104
Db 1 AGCCATTGAGAGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 60
Qy 1105 AGATGAGATCTGCTGCTGCGCCAGGCTGAGTGAAGCGGCGTATCAAGTCACTGACG 1164
Db 61 AAGAGATCTCACTCTCTGCTGCGCCAGGCTGAGTGAAGCGGCGTATCAAGTCACTGACG 120
Qy 1165 CCTCAACCTTCTAGAGCTCAAGGAGATTCTCCACCTCAGGCTCCCAAGTATGGAGCAAC 1224
Db 121 CCTCGGCCCCCAGGTTCAAGGAGATTCTGCTGCTGAGCTCCCTAGTATGAGTAATTAC 180

Qy 1225 ACGTATGCGCCACCATGCTGCTAATTTCTAATTTTGTAGATAGATCTCACTA 1284
Db 181 AGGCAACCTGCCACATGCACTGCTGCTAATTTTGTATTTTAAATAGAGACAGGCTTTCACCA 240
Qy 1285 TATTTGTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
Db 241 TGTTCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 1345 AAGTACGAGATTACAGGATGAGGCAAGGCTCCCTGCGCCATATGAGATTTT 1396
Db 301 AAGTCTGGATTAAGGATGAGGCAAGGCTCCCTGCGCCATATGAGATTTT 352

RESULT 12
B2604977 762 bp DNA linear GSS 08-JUN-2003
LOCUS B2604977/c
DEFINITION WHAIV58TR Human MCF7 breast cancer cell line library (MCF7_1) Homo
sapiens genomic clone MCF7_1-6120, genomic survey sequence.
ACCESSION B2604977
VERSION B2604977.1 GI:31513534
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Negrange, G., de Jong, P.,
Gray, J.W. and Collins, C.
TITLE End-sequence profiling: Sequence-based analysis of aberrant genomes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
PUBMED 12788976
COMMENT Contact: Volik SV
Collin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.

FEATURES
source
1..762
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-6120"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library
[MCF7_1]"
/note="Vector: pGEM-BAC1; Site 1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (http://www.genomex.com) using their standard
procedure."

ORIGIN
Query Match 5.7%; Score 204; DB 9; Length 762;
Best Local Similarity 74.1%; Pred. No. 7.5e-22;
Matches 258; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1049 AATACAGGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1108
Db 703 AAAACCTGCTTCTTCT 644
Qy 1109 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1168
Db 643 GGTGTTGCTCTCTCAACCAAGCTGAGTGAAGTGTGCAATCAAGCTCACTGAGTCTT 584
Qy 1169 AACCTTGAAGCTCAAGGATTTCTCCACCTCAGGCTCCCAAGTATGGAGCAACAT 1228
Db 121 CCTCGGCCCCCAGGTTCAAGGAGATTCTGCTGCTGAGCTCCCTAGTATGAGTAATTAC 180

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Db      563 AACCTCCAGGCCCCAGCAATCTCTCCCAATTACGCTCCCAAGTACTTGACACACAGGC 524
Qy      1229 ATGCCCAACCATGCTGCTAAATTTCTATTTTGTAGAGATAGATCTCATATAT 1288
Db      523 ATGTGCACCATGCTGCTATTTTGTATTTTGTAGAGATAGGAGTTTCACTATGCT 464
Qy      1289 GTTCAGGCTGCTGTGAATTCCTGGGCTCAGGTAGCTCCCACTCGGGCTTCCCAAT 1348
Db      463 GCCCAGGCTGCTCAAACTCTCGGGCTCAGAGCATATTCACCTTACCTTCCCAAGT 404
Qy      1349 ACTGGATTATACGAGCATGAGCCAGAGGTCCCTGCCCATATGAGATTTT 1396
Db      403 GCTGGATTACAGGCAATGAGCCAGCTATCCCACTTAATGACTTT 356

RESULT 13
LOCUS   AM089016/c 352 bp mRNA linear EST 15-OCT-1999
DEFINITION xtd3402.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595651 3'
similar to contains Alu repetitive element; contains element HGR
repetitive element ;, mRNA sequence.
ACCESSION AM089016
VERSION   AM089016.1 GI:6044851
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 352)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL   Tumor Gene Index
COMMENT    Unpublished (1997)
Email: cgapb-remail.nih.gov
Contract: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 321.
FEATURES
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                /db_xref="taxon:9606"
                /clone="IMAGE:2595651"
                /tissue_type="tumor, 5 pooled (see description)"
                /lab_host="DH10B"
                /clone_1ib="NCI_CGAP_Ov23"
                /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
                Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.35 kb. Tumor types include: mixed
                Mullerian tumor, papillary serous, clear cell, spindle
                cell. All are primary tumors, metastasis positive. Life
                Technologies catalog #: 11534-013"

ORIGIN
Query Match 5.7%; Score 203.8; DB 1; Length 352;
Best Local Similarity 76.5%; Pred. No. 9.7e-22;
Matches 250; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy      1072 TTTTAAATTTATTTATTTATTTATTTTGAAGATGAGTCTGCTGCCAGGCT 1131
Db      337 TAGATATGATATGATATTTATTTATTTTGAAGGAGATCTGCTGACCCAGGCT 278
Qy      1132 GAGAGCAGCGGGGATCAAGTTCACTGACGCTCAACCTTCAGGCTCAAGGATTC 1191

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Db      277 GAGATGCAATGACAGATCTCGGCTCACTACAACTCTGCTTGGGTTCAAGTATTC 218
Qy      1192 TCCCACTCAGCCCCCAAGTAGTTGGACCAACGATATGCCCAACATGCTGCTAAT 1251
Db      217 TCCCACTCAGCTCTGATGATGCTGGATATCAAGGATAGCGCCAGACTCTGCTAAT 158
Qy      1253 TTCTATTTTGTAGAGATAGATCTCATATTTGTCCAGGCTGTGATTTCT 1311
Db      157 TTTTGTATTTTGTAGAGATAGGAGTTTCACATTTTACCAAGCTGTGTAATCT 98
Qy      1312 GGGCTCAGGTAGCTCTCCCACTGGGAGCTCCCAAGTACTGGGATTACAGGATAGCCA 1371
Db      97 GACTCTAGGTATATTCACCACTTGGCTTCCCAAGTGTGGATTACAGGATAGCCA 38
Qy      1372 AGTCCCTGCCCCATATGAGATTTTCT 1398
Db      37 CTGTGCGCGGCTCATTTTTTTTTT 11

RESULT 14
LOCUS   AG132086 656 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-144F15.R, genomic survey sequence.
ACCESSION AG132086
VERSION   AG132086.1 GI:16661764
KEYWORDS GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
REFERENCE 1
AUTHORS   Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLES    BAC end sequences of library PTB
JOURNAL   Unpublished
COMMENT    2 (bases 1 to 656)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22, Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpes@gsr.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
FEATURES
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            R.Site 2 : SacI.
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                    /db_xref="taxon:9598"
                    /clone="PTB-144F15.R"
                    /sex="male"
                    /cell_type="lymphoblast"
                    /clone_1ib="PTB Chimpanzee Male BAC Library"

ORIGIN
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Matches 259; Conservative 0; Mismatches 73; Indels 2; Gaps 1;

Qy      1060 TTAATTTTATTTATTTATTTATTTATTTATTTTGAAGATGAGTCTG-- 1117
Db      73 TAGATATGACGCTTATTTATTTATTTATTTATTTATTTATTTAGACAGAGTCTGCT 132

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DR P-PSDB; AAW31850.

XX New isolated human eosinophil eotaxin receptor - used to develop products
PT for treating and preventing atopic conditions e.g. allergic rhinitis,
PT dermatitis, conjunctivitis and bronchial asthma.

XX Claim 12, 13, 14; Page 16-20; 51pp; English.

XX This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil eotaxin receptor protein. Flanked by a 5'
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for the
CC treatment and prevention of atopic conditions such as allergic rhinitis,
CC dermatitis, conjunctivitis and bronchial asthma. Agents which block this
CC eosinophil eotaxin receptor can be used to prevent viral infection in
CC healthy individuals and slow or halt viral progression in infected
CC patients

CC Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T; 0 U; 0 Other;

Query Match 100.0%; Score 3586; DB 2; Length 5099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAATCCCTACCTCCCATCAGAGCTAAGGGGAGTGAAGCGCTCTCTGCTAAGATGGGA 60
DB 1 GGAATCCCTACCTCCCATCAGAGCTAAGGGGAGTGAAGCGCTCTCTGCTAAGATGGGA 60
QY 61 CCCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACCAATGGATGGCCAGTGGGTT 120
DB 61 CCCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACCAATGGATGGCCAGTGGGTT 120
QY 121 AAGTTGTGTGTGAGGAGAAAAAAGATCTAGTTTGTACTCTGTGAGATCTCTGGTT 180
DB 121 AAGTTGTGTGTGAGGAGAAAAAAGATCTAGTTTGTACTCTGTGAGATCTCTGGTT 180
QY 181 GTTCATGTGATGGGAGAGTCAAGAGACAGAGCTTGCTCAGTGGCTCAAGTGA 240
DB 181 GTTCATGTGATGGGAGAGTCAAGAGACAGAGCTTGCTCAGTGGCTCAAGTGA 240
QY 241 GGAAGAGTGCATAGCTTGGGCGAAGGCGCAAGGCTGTGTGAGAGCGTATGGTAA 300
DB 241 GGAAGAGTGCATAGCTTGGGCGAAGGCGCAAGGCTGTGTGAGAGCGTATGGTAA 300
QY 241 GGAAGAGTGCATAGCTTGGGCGAAGGCGCAAGGCTGTGTGAGAGCGTATGGTAA 300
DB 241 GGAAGAGTGCATAGCTTGGGCGAAGGCGCAAGGCTGTGTGAGAGCGTATGGTAA 300
QY 301 GAGGCTCTCCATCCAGGCCCAAGAACTAAGTAATCACTCATAGATATTTAGC 360
DB 301 GAGGCTCTCCATCCAGGCCCAAGAACTAAGTAATCACTCATAGATATTTAGC 360
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DB 361 TACAAACACACAGAGGTTCCAGAAAAAGGCTCAGCTTGGAAACAGTCAACCCCA 420
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DB 421 TCAGCAGACACAGATATTAATCAAGAACCAAGAGACAGAAACCCCTTCCCA 480
QY 481 CTCTGCCCCATGTCTCAAGTTGAGTGGCCCTTCTCCAGATCTTGCAACCACTTTAA 540
DB 481 CTCTGCCCCATGTCTCAAGTTGAGTGGCCCTTCTCCAGATCTTGCAACCACTTTAA 540
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QY 721 GTTTGAGACATAAAGATCATTTGACATTTGACATGCTGAGTTGTATTTGTAGTAATTTTA 780
DB 721 GTTTGAGACATAAAGATCATTTGACATTTGACATGCTGAGTTGTATTTGTAGTAATTTTA 780
QY 781 GTTGAACCTCATTTTGTAAATCTTGACACAGGGGGCAATCCAAATCTGACAAAGATATG 840
DB 781 GTTGAACCTCATTTTGTAAATCTTGACACAGGGGGCAATCCAAATCTGACAAAGATATG 840
QY 841 TTAACAGATGTAATGCTGACATGAGAGATTTGGTGAATTTTACTTCTGTTTTGTCT 900
DB 841 TTAACAGATGTAATGCTGACATGAGAGATTTGGTGAATTTTACTTCTGTTTTGTCT 900
QY 901 CTCTCTTCTTATTTGCTTACTTATTTAGATTAATCACTATGCTTTTCCAAATGTAAA 960
DB 901 CTCTCTTCTTATTTGCTTACTTATTTAGATTAATCACTATGCTTTTCCAAATGTAAA 960
QY 961 GGGCAATTTGAAAGCTTAATCAAACTCTTCACTATTTTGTAAATGATATTCACCTG 1020
DB 961 GGGCAATTTGAAAGCTTAATCAAACTCTTCACTATTTTGTAAATGATATTCACCTG 1020
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QY 1081 ATTATATTTATTTATTTTATTTTGAATGAGTCTGCTGCTGCCAGGCTGAGTGCAG 1140
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QY 1141 CGGCGTATCAACATTTCACTGACAGCTCAACCTTTAGGCTCAAGGATTTCCCACTC 1200
DB 1141 CGGCGTATCAACATTTCACTGACAGCTCAACCTTTAGGCTCAAGGATTTCCCACTC 1200
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DB 1201 AGCCCCCAAGATGTTGGGACCAACAGTATGCGCACCATGCTGGCTAATTTCTAAT 1260
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DB 1261 TTTGTGAAGATGAGATCTCACTATATTTGTCAGGCTGGTCTTGAATTCCTGGCTCAG 1320
QY 1321 TGAAGCTCCCACTGGGCTCCCAAGATGCGGATTAAGGCAAGACAGAGTCCCT 1380
DB 1321 TGAAGCTCCCACTGGGCTCCCAAGATGCGGATTAAGGCAAGACAGAGTCCCT 1380
QY 1381 GGCATATGAGATTTTCTGTCTGATCCCATGACGTAAGTAAAGGACTGGCTCT 1440
DB 1381 GGCATATGAGATTTTCTGTCTGATCCCATGACGTAAGTAAAGGACTGGCTCT 1440
QY 1441 GACTGTGAGAGCTGCAATGCTTTCTTGAAGTGTGAACCTTCAAGTCTAAAGCTCATAG 1500
DB 1441 GACTGTGAGAGCTGCAATGCTTTCTTGAAGTGTGAACCTTCAAGTCTAAAGCTCATAG 1500
QY 1501 CAGCCCTGAACCCCAACCAAAAGGTTCAATGTTTATCAATCCATGATATTTTA 1560
DB 1501 CAGCCCTGAACCCCAACCAAAAGGTTCAATGTTTATCAATCCATGATATTTTA 1560
QY 1561 TAGAATTAACATGATATTAAGACATACCTCAACCTGAGCAAACTTAAGTAATTT 1620
DB 1561 TAGAATTAACATGATATTAAGACATACCTCAACCTGAGCAAACTTAAGTAATTT 1620
QY 1621 TTTAAAGTTTGAACCTGTTTTTAAATCACTTGTGAAGAAAAAGAAATTAATATCAATA 1680
DB 1621 TTTAAAGTTTGAACCTGTTTTTAAATCACTTGTGAAGAAAAAGAAATTAATATCAATA 1680
QY 1681 TTAAGGATGATATGAGGCTATATCTTTTGTCTTCCAGATTTACAGTCTGTTCTTT 1740
DB 1681 TTAAGGATGATATGAGGCTATATCTTTTGTCTTCCAGATTTACAGTCTGTTCTTT 1740
QY 1741 CTGTGCTTAAGATGCTGAAGTGAAGAGCACTGTGATTTGTACGTGTATCTGACAA 1800
DB 1741 CTGTGCTTAAGATGCTGAAGTGAAGAGCACTGTGATTTGTACGTGTATCTGACAA 1800

QY 1801 AATGTAATTTTTTCTCAGCTGCTATGATGTAATGCTATTAATGATTAAGAAATGC 1860
 DB 1801 AATGTAATTTTTTCTCAGCTGCTATGATGTAATGCTATTAATGATTAAGAAATGC 1860
 QY 1861 TGAATGGAGACACACAAACATTTGTTCTCAGTTCATTTTCTCTCTCAAAAGCTGGA 1920
 DB 1861 TGAATGGAGACACACAAACATTTGTTCTCAGTTCATTTTCTCTCTCAAAAGCTGGA 1920
 QY 1921 ATGTCCATTTGATCAGTGGAGATGTAACCTGACAGACCAATGAAAGATCAACAAGT 1980
 DB 1921 ATGTCCATTTGATCAGTGGAGATGTAACCTGACAGACCAATGAAAGATCAACAAGT 1980
 QY 1981 TCACCCAAAGGAGACCTATTTTCTTAATTTCAATTTGAATGAGCTTCTAATTTGCTTCT 2040
 DB 1981 TCACCCAAAGGAGACCTATTTTCTTAATTTCAATTTGAATGAGCTTCTAATTTGCTTCT 2040
 QY 2041 TTCAATTCCTGCTTCTCAACAGTTTTCAGCTTTTCTGTTTCAAAATGAACTCAGATA 2100
 DB 2041 TTCAATTCCTGCTTCTCAACAGTTTTCAGCTTTTCTGTTTCAAAATGAACTCAGATA 2100
 QY 2101 CACTCTCAATTTTCTCAACAGTTTTCAGCTTTTCTGTTTCAAAATGAACTCAGATA 2160
 DB 2101 CACTCTCAATTTTCTCAACAGTTTTCAGCTTTTCTGTTTCAAAATGAACTCAGATA 2160
 QY 2161 GTAAAGAGAGCTCTGCAATTAAGAGCTTGTCCAAAGGACGACGCTGAGAGCGCTAGACT 2220
 DB 2161 GTAAAGAGAGCTCTGCAATTAAGAGCTTGTGTCCAAAGGACGACGCTGAGAGCGCTAGACT 2220
 QY 2221 GGCTCAATTTCTCAATCTATTTCTCACTGACCTTGAACCTCAAGAACCCCAACATGTGGG 2280
 DB 2221 GGCTCAATTTCTCAATCTATTTCTCACTGACCTTGAACCTCAAGAACCCCAACATGTGGG 2280
 QY 2281 CCTCAGATTTGATCAATTTATTTTAAGAAAGCAAAACATTTCCCGCATTTGGCCCA 2340
 DB 2281 CCTCAGATTTGATCAATTTATTTTAAGAAAGCAAAACATTTCCCGCATTTGGCCCA 2340
 QY 2341 GTTATTAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGGCTGTATTTCAATTC 2400
 DB 2341 GTTATTAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGGCTGTATTTCAATTC 2400
 QY 2401 TTCAACCTTGTCTCTCTCTCAAGAAAGAGAAAGTCAAGTTGATGCTCTGAGAACT 2460
 DB 2401 TTCAACCTTGTCTCTCTCTCAAGAAAGAGAAAGTCAAGTTGATGCTCTGAGAACT 2460
 QY 2461 AGTGCATGCTTAATCTGCTTCTCAAGAAATGCCATGGGCTGTATTTCAATTTCTCTCT 2520
 DB 2461 AGTGCATGCTTAATCTGCTTCTCAAGAAATGCCATGGGCTGTATTTCAATTTCTCTCT 2520
 QY 2521 TTTCACCGAAGCTATTAATCTCAAGAAAGAGCACTGGCTTGAAGGCTCTGAGCTA 2580
 DB 2521 TTTCACCGAAGCTATTAATCTCAAGAAAGAGCACTGGCTTGAAGGCTCTGAGCTA 2580
 QY 2581 AGAAATATCAAGTCCAGTGAAGAAATCCATGACCTGACCTCTGCTTATACCTCTTGTG 2640
 DB 2581 AGAAATATCAAGTCCAGTGAAGAAATCCATGACCTGACCTCTGCTTATACCTCTTGTG 2640
 QY 2641 ATGAGAGAGCTCCAGGGGTTTCTTTTTCATGTTTCAAGGCTTAACTACAGATCAACA 2700
 DB 2641 ATGAGAGAGCTCCAGGGGTTTCTTTTTCATGTTTCAAGGCTTAACTACAGATCAACA 2700
 QY 2701 GGGGGCAAGAAAGAAAGTAACTAACTAATGCTGCTTAAATTTAATTTAATTTAAT 2760
 DB 2701 GGGGGCAAGAAAGAAAGTAACTAACTAATGCTGCTTAAATTTAATTTAATTTAATTTAAT 2760
 QY 2761 GTTAATTAATCTGATTTGAATGATGTAACAGACAAATGTAATTTTTCACAGCTGCT 2820
 DB 2761 GTTAATTAATCTGATTTGAATGATGTAACAGACAAATGTAATTTTTCACAGCTGCT 2820
 QY 2821 GTGAGATGATTAATGCAATTTGGAATTAAGAAATGCTTTAAGAGCAACAAGCGATTC 2880
 DB 2821 GTGAGATGATTAATGCAATTTGGAATTAAGAAATGCTTTAAGAGCAACAAGCGATTC 2880
 QY 2881 TCAAGTCCGTAAGCAATTTTCAAAAGTTAAATTTAAATTCATCAATTTGAATCTAGT 2940

DB 2881 TCAGATCCGTAGCAATTTTTCAAAAGTTAAATTTAAATATCAATCAATTTGAATCTAGT 2940
 QY 2941 GACAGAGAAATGACATGATTAAGAGACTAAAGATCTAGCCCAATTTTATTAATTAATCTG 3000
 DB 2941 GACAGAGAAATGACATGATTAAGAGACTAAAGATCTAGCCCAATTTTATTAATTAATCTG 3000
 QY 3001 TTAGAGATTTTGAACAAATTAATTAATTTCTTCAAGGTTCAATTTCCCATTAATCTATA 3060
 DB 3001 TTAGAGATTTTGAACAAATTAATTAATTTCTTCAAGGTTCAATTTCCCATTAATCTATA 3060
 QY 3061 ATGAATGCTCATCTTAATGAGGCTCTGAGAGAGCTAATTAATTTGTAATTAATC 3120
 DB 3061 ATGAATGCTCATCTTAATGAGGCTCTGAGAGAGCTAATTAATTTGTAATTAATC 3120
 QY 3121 ATTTGTAATTAATTAATTAATTAATTTTGTGCTTTAAATGATTAAGTAAATTAATG 3180
 DB 3121 ATTTGTAATTAATTAATTAATTAATTTTGTGCTTTAAATGATTAAGTAAATTAATG 3180
 QY 3181 TAACTGTAATTAATTAATTAATTAATGCGCTAAGAGACATGATTAATTAATTAATTAAT 3240
 DB 3181 TAACTGTAATTAATTAATTAATTAATGCGCTAAGAGACATGATTAATTAATTAATTAAT 3240
 QY 3241 TAAATTTGTAATTAATTAATTAATGCTGTTTCTGTTGTAATTTCTTAAATGCT 3300
 DB 3241 TAAATTTGTAATTAATTAATTAATGCTGTTTCTGTTGTAATTTCTTAAATGCT 3300
 QY 3301 TACAGAAATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3360
 DB 3301 TACAGAAATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3360
 QY 3361 ATGCGGCTCATCTAATTTGAAGCTTCTTCTCTCAATCTTCTCTGAGC 3420
 DB 3361 ATGCGGCTCATCTAATTTGAAGCTTCTTCTCTCAATCTTCTCTGAGC 3420
 QY 3421 ACCCTGTAATGCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3480
 DB 3421 ACCCTGTAATGCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3480
 QY 3481 CATCTTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3540
 DB 3481 CATCTTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3540
 QY 3541 CATGAGGATTAATTTTCTTCTTCAATCAAGGAGAGATGAA 3586
 DB 3541 CATGAGGATTAATTTTCTTCTTCAATCAAGGAGAGATGAA 3586

RESULT 2
 ID ABZ68879 strand: cDNA; 5791 BP.
 AC ABZ68879;
 DT 28-MAY-2003 (first entry)
 XX
 DB Nucleotide sequence of human chemokine receptor CCR3.
 XX Human; chemokine receptor; CCR3; viral infection; surface protein;
 KW respiratory virus infection; respiratory syncytial virus infection;
 KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma; gene; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 4015..5082
 FT /tag= a
 FT /product= "CCR3"
 PN MO2003014153-A2.
 XX
 XX 20-FEB-2003.

PF 12-AUG-2002; 2002MO-CA001248.
 XX 10-AUG-2001; 2001US-0311088P.
 XX (TOPI-) TOPIGEN PHARM INC.
 PA Renzi P, Zemzouni K;
 XX WPI; 2003-256541/25.
 DR P-PSDB; ABP97726.
 XX
 PT Modulating viral infection of a cell, for treating or preventing
 PT respiratory virus infections, bronchitis, pneumonia or asthma, by
 PT modulating a binding interaction between a cell chemokine-receptor and a
 PT surface protein of the virus.
 XX
 XX Disclosure; Page 84-88; 120pp; English.
 CC The present sequence encodes human chemokine receptor CCR3. The
 CC specification describes a method for modulating viral infection of a
 CC cell. The method comprises modulating a binding interaction between a
 CC cell chemokine-receptor and a surface protein of the virus. The proviso
 CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
 CC not HIV. The method is useful for treating or preventing respiratory
 CC virus infection in vertebrates, more particularly respiratory syncytial
 CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
 CC bronchitis, pneumonia or asthma
 CC
 SQ Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 97.4%; Score 3494.4; DB 8; Length 5791;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

QY 1 GGATCCCTACCTCCCATCAGAGCTAGGGGCGATGAGCGCTCTGCTAAGATGAGGA 60
 DB 433 GGATCCCTACCTCCCATCAGAGCTAGGGGCGATGAGCGCTCTGCTAAGATGAGGA 492
 QY 61 CCCCAAGAAATGTCTCCCTGTGGGCACTTCTTAACAATGGATGGCAAGTGGGTT 120
 DB 493 CCCCAAGAAATGTCTCCCTGTGGGCACTTCTTAACAATGGATGGCAAGTGGGTT 552
 QY 121 AAGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 DB 553 AAGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
 QY 181 GTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 DB 613 GTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
 QY 241 GGAAGAGGTGATAGGCTGGGCGAGGGCGAGGGCCCTGTGTGAGAGGCGTATGATGAT 300
 DB 673 GGAAGAGGTGATAGGCTGGGCGAGGGCGAGGGCCCTGTGTGAGAGGCGTATGATGAT 732
 QY 301 GAGGGCTCTCCATTCAGGCCCAAGAGACTAAGATGAATCTCATAGATATATTAC 360
 DB 733 GAGGGCTCTCCATTCAGGCCCAAGAGACTAAGATGAATCTCATAGATATATTAC 792
 QY 361 TACAACACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
 DB 793 TACAACACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 852
 QY 421 TCAGCAGACCAAGATCATATAATCAAGACCAAGACCAAGACCAAGACCAAGACCAAGAC 480
 DB 853 TCAGCAGACCAAGATCATATAATCAAGACCAAGACCAAGACCAAGACCAAGACCAAGAC 912
 QY 481 CTCTGCCCCATGTCTCAAGTTGATGAGGCCCTTCTCCAGATCTTCCCAACATCTTAA 540
 DB 913 CTCTGCCCCATGTCTCAAGTTGATGAGGCCCTTCTCCAGATCTTCCCAACATCTTAA 972
 QY 541 AAGGAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 DB 973 AAGGAACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1032

QY 601 ACCCTAAATCATTTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 1033 ACCCTAAATCATTTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1092
 QY 661 TGTGTGAATCTTTTCTGCTATCCAGAGATGAGAGTGTGTAAACAGACCAATTA 720
 DB 1093 TGTGTGAATCTTTTCTGCTATCCAGAGATGAGAGTGTGTAAACAGACCAATTA 1152
 QY 721 GTTTGAGACCTAAGAAATCAATTCACATTCCTGAGTTGATGTGATGATTTTA 780
 DB 1153 GTTTGAGACCTAAGAAATCAATTCACATTCCTGAGTTGATGTGATGATTTTA 1212
 QY 781 GTTGAACCTCAC-TTTGTAAATCTTGACACAGGGGAAATCCAAATCTCCACAAAGAT 839
 DB 1213 GTTGAACCTCAC-TTTGTAAATCTTGACACAGGGGAAATCCAAATCTCCACAAAGAT 1268
 QY 840 GTTAAACAGAGTGAATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 899
 DB 1269 GTTAA-CAAGTGTAAATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1327
 QY 900 TCTTCTTCTTATTTGTTCTTAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 959
 DB 1328 TCTTCTTCTTATTTGTTCTTACTTATTAATTAATTAATTAATTAATTAATTAATTAAT 1386
 QY 960 AGGCCATTTTGAAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1019
 DB 1387 AGGCCATTTTGAAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1446
 QY 1020 GATTGAGCTGGGTGAGCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1079
 DB 1447 GATTGAGCTGGGTGAGCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1506
 QY 1080 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1139
 DB 1507 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1566
 QY 1140 GGGGCTGATCAAGTTCACTGACGCTCAACCTTTAGGCTCAAGGAGATCTCCACCT 1199
 DB 1567 GGGGCTGATCAAGTTCACTGACGCTCAACCTTTAGGCTCAAGGAGATCTCCACCT 1626
 QY 1200 CAGCCCCCAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1259
 DB 1627 CAGCCCCCAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1686
 QY 1260 TTTTGTAGATAGATCTCATATATTTGTCAGAGTGTCTGATTAATCTGGGCTGAG 1319
 DB 1687 TTTTGTAGATAGATCTCATATATTTGTCAGAGTGTCTGATTAATCTGGGCTGAG 1746
 QY 1320 GTGAGCTTCCACCTGGGCTTCCCAAGTATGAGGAGTTACAGGAGTACAGGAGTCC 1379
 DB 1747 GTGAGCTTCCACCTGGGCTTCCCAAGTATGAGGAGTTACAGGAGTACAGGAGTCC 1806
 QY 1380 TGCCCATATAGATTTTGTGCTGATCTCAATGAGGAGTATCAAGGAGCTTGGGCTGC 1439
 DB 1807 TGCCCATATAGATTTTGTGCTGATCTCAATGAGGAGTATCAAGGAGCTTGGGCTGC 1866
 QY 1440 TGACTCTGAGAGACCTGATAGCTTTCTTGAAGTGTGAACCTTCAAGTGTAAAGCTCAT 1499
 DB 1867 TGACTCTGAGAGACCTGATAGCTTTCTTGAAGTGTGAACCTTCAAGTGTAAAGCTCAT 1926
 QY 1500 GCAAGCTTGAAGCCCAACCAAAAGTGTATGTTTATCATCTGATCAATTTGATTTT 1559
 DB 1927 GCAAGCTTGAAGCCCAACCAAAAGTGTATGTTTATCATCTGATCAATTTGATTTT 1986
 QY 1560 ATAGAAATPAACATGAATTAAGACATACCTCAACCTGAGCAAACTTAAGTAAATTT 1619
 DB 1987 ATAGAAATPAACATGAATTAAGACATACCTCAACCTGAGCAAACTTAAGTAAATTT 2046
 QY 1620 TTTTAAAGTTGACCTGTTTTTAAATCACTCTTGAGAGGAGGAGGAGGAGGAGGAGGAG 1679
 DB 2047 TTTTAAAGTTGACCTGTTTTTAAATCACTCTTGAGAGGAGGAGGAGGAGGAGGAGGAG 2106

QY 1680 ATTAACGCTGAATACAGGCTACTATACCTTTGTTCTCAGAAATTAGCAGTCTGTCTTT 1739
DB 2107 ATTAACGGGAAATACAGGCTACTATACCTTTGTTCTCAGAAATTAGCAGTCTGTCTTT 2166
QY 1740 TCTTGCTTTAGATGCTGAAGTGCAGAAAGACACTCTGTGTATTTGATGCTGTATCTGACA 1799
DB 2167 TCTTGCTTTAGATGCTGAAGTGCAGAAAGACACTCTGTGTATTTGATGCTGTATCTGACA 2226
QY 1800 AAATGATATTTTCTCAGCTGCTATGATTTGATTTATGCTATTTATGATTAAGAAATG 1859
DB 2227 AAATGATATTTTCTCAGCTGCTATGATTTGATTTATGCTATTTATGATTAAGAAATG 2286
QY 1860 CTGATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCTG 1919
DB 2287 CTGATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCTG 2346
QY 1920 AATGTCCTATGATCAGTGGAGATGATCTGTGACAGACCCATGAAAGATCAACAG 1979
DB 2347 AATGTCCTATGATCAGTGGAGATGATCTGTGACAGACCCATGAAAGATCAACAG 2406
QY 1980 TTCCACCCGAGGAGCCCTATTTTCTATTTCAATTTGAATGGCTTCTAATTTGCTTC 2039
DB 2407 TTCCACCCGAGGAGCCCTATTTTCTATTTCAATTTGAATGGCTTCTAATTTGCTTC 2466
QY 2040 TTTCAATCTGCTCTTACCAAGTTTACAGCTTTTCTGCTTCAATGTAATCTGACAT 2099
DB 2467 TTTCAATCTGCTCTTACCAAGTTTACAGCTTTTCTGCTTCAATGTAATCTGACAT 2526
QY 2100 AACCTCTCATTTTCTCTCATCAACACCCCAAGTACCCCAATGCTCTCATTTGATAT 2159
DB 2527 AACCTCTCATTTTCTCTCATCAACACCCCAAGTACCCCAATGCTCTCATTTGATAT 2586
QY 2160 AATAAAGAGGCTGCTGCAATTAAGGGCTTTCAGAGGACGAGCTAGAGGGCTGAGAC 2219
DB 2587 AATAAAGAGGCTGCTGCAATTAAGGGCTTTCAGAGGACGAGCTAGAGGGCTGAGAC 2646
QY 2220 TGGCTCCATTTTCACTATTTCTCACTGACTTGTGACTACCCGAAACCCCAATG 2279
DB 2647 TGGCTCCATTTTCACTATTTCTCACTGACTTGTGACTACCCGAAACCCCAATG 2706
QY 2280 GCTCAGATTCGATCAATTTATTTATTAAGAAAGAAACAAATTTCCCGCATTTGCCCC 2339
DB 2707 GCTCAGATTCGATCAATTTATTTATTAAGAAAGAAACAAATTTCCCGCATTTGCCCC 2766
QY 2340 AGTATTAAGCAATTTCTCAGATTTTACCTTGAAGAAAGCCCAATGGCTGTATTTACAT 2399
DB 2767 AGTATTAAGCAATTTCTCAGATTTTACCTTGAAGAAAGCCCAATGGCTGTATTTACAT 2826
QY 2400 CTTCACCTTGTCCCTTCTCTCAGAAAGGAAAGTCAAGTTGATGCTCTGAGAAAC 2459
DB 2827 CTTCACCTTGTCCCTTCTCTCAGAAAGGAAAGTCAAGTTGATGCTCTGAGAAAC 2886
QY 2460 TAGTGATGGCTTAACTGTCTCTCATGACTCTGCTTATCTGTTTTCTATTTTCTCC 2519
DB 2887 TAGTGATGGCTTAACTGTCTCTCATGACTCTGCTTATCTGTTTTCTATTTTCTCC 2946
QY 2520 TTTTTCACCGAAGTCTAATATCTCAAGAAAGAGGACCTGCTTAAAGGCTCTGCTCC 2579
DB 2947 TTTTTCACCGAAGTCTAATATCTCAAGAAAGAGGACCTGCTTAAAGGCTCTGCTCC 3006
QY 2580 AAGAAATATCAAGTCCAGTGAAGAAATCCCATGACACCCCTCTGCTTAAAGGCTCTGCT 2639
DB 3007 AAGAAATATCAAGTCCAGTGAAGAAATCCCATGACACCCCTCTGCTTAAAGGCTCTGCT 3066
QY 2640 GATGAGAAAGCTCCAGGAGGTTTGTCTTTTTCAGTGTACAGGCTTAACTCAGATCAC 2699
DB 3067 GATGAGAAAGCTCCAGGAGGTTTGTCTTTTTCAGTGTACAGGCTTAACTCAGATCAC 3126
QY 2700 AAGGAGGAAAGAAAGAAAGTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2759
DB 3127 AAGGAGGAAAGAAAGAAAGTAACTTAACTTAACTTAACTTAACTTAACTTAACT 3186
QY 2760 AGTTAATTACTGATTTGTATCATGTGTAAACAGCAAAATGTGTATTTTTCACAGCTGC 2819

DB 3187 AGTTAATTACTGATTTGTATCATGTGTAAACAGCAAAATGTGTATTTTTCACAGCTGC 3246
QY 2820 TGTGATGGAATTAATGCAATTTGAAATAGAAATGCTTTAAGACACACAGGCTGCTC 2879
DB 3247 TGTGATGGAATTAATGCAATTTGAAATAGAAATGCTTTAAGACACACAGGCTGCTC 3306
QY 2880 CTCAAGTCCGATGCAAAATTTTCAAAAGTTAAATTTAAATCACTACATTTGAATCTAG 2939
DB 3307 CTCAAGTCCGATGCAAAATTTTCAAAAGTTAAATTTAAATCACTACATTTGAATCTAG 3366
QY 2940 TGAACGAGAAATGACATGATATAGACTTAAAGATCTAGCCCAATTTTATTTACTT 2999
DB 3367 TGAACGAGAAATGACATGATATAGACTTAAAGATCTAGCCCAATTTTATTTACTT 3426
QY 3000 GTTAGAGATTTTGAACAAATTAATTAATTTCTGCAAGGTTCAATTTCCCATTAATCTAT 3059
DB 3427 GTTAGAGATTTTGAACAAATTAATTAATTTCTGCAAGGTTCAATTTCCCATTAATCTAT 3486
QY 3060 AATGAAATGCTCATCATTAATGAGGAGCTGAGAGAGCATTAATTTGATTAATTAAT 3119
DB 3487 AATGAAATGCTCATCATTAATGAGGAGCTGAGAGAGCATTAATTTGATTAATTAAT 3546
QY 3120 CATGTTATTAATTAATTAATTAATTTGCTTTTAAATGATTAAGATTTTAAAGTATAT 3179
DB 3547 CATGTTATTAATTAATTAATTAATTTGCTTTTAAATGATTAAGATTTTAAAGTATAT 3606
QY 3180 GTTAACTGTAAACATTAATTAATTAATGCTTAAATGAGACAGTAAATTAATTAATTAAT 3239
DB 3607 GTTAACTGTAAACATTAATTAATTAATGCTTAAATGAGACAGTAAATTAATTAATTAAT 3666
QY 3240 TTATATTTTATCATTAATTAATTAATTTTCTGTTGATTTTCTTCTTAAATG 3299
DB 3667 TTATATTTTATCATTAATTAATTAATTTTCTGTTGATTTTCTTCTTAAATG 3726
QY 3300 TTAAGAAATCTGTATCTCCATTTTCTTACACCAACCAACCAATTTGCTTCTTTTCC 3359
DB 3727 TTAAGAAATCTGTATCTCCATTTTCTTACACCAACCAACCAATTTGCTTCTTTTCC 3786
QY 3360 CATGCC-GGTGATGCTAATTTTGAAGAGCTTCAAGCTTCTTCTTCAATCTTCTCCG 3418
DB 3787 CATGCCGAGTGTATGCTTAAAGAGCTTCAAGCTTCTTCTTCAATCTTCTCCG 3846
QY 3419 GCACCTCTGATTAATGCTTTTGAATTTTCTTCTTATCAACAGGAGAAAGTAA 3478
DB 3847 GCACCTCTGATTAATGCTTTTGAATTTTCTTCTTATCAACAGGAGAAAGTAA 3906
QY 3479 GGCATCTTGTGATGATTAATTAATCACTGCTGTGTTTTTACAGAGATTAATG 3538
DB 3907 GGCATCTTGTGATGATTAATTAATCACTGCTGTGTTTTTACAGAGATTAATG 3966
QY 3539 TTCAATTTGAGATTAATTTTCTTCTTATCAACAGGAGAAAGTAA 3586
DB 3967 TTCAATTTGAGATTAATTTTCTTCTTATCAACAGGAGAAAGTAA 4014

RESULT 3
ADY86631
ID ADY86631 standard; DNA, 5791 bp.
XX
XX ADY86631;
XX
XX 02-JUN-2005 (first entry)
XX
XX Human CC chemokine receptor 3 (CCR3) gene.
XX
XX Gene expression; screening; multiple sclerosis; neuroprotective;
XX
XX immune disorder; neurological disease; DNA microarray; gene; ds;
XX
XX chemokine.
XX
XX Homo sapiens.
XX
XX US2005064483-A1.
XX
XX

QY	1650	TTTTAAAGTTGACCGTGTTTTTAAATCACTCTGGAGAAAAAGAAAAATTAATCAATA	1679
Db	2047	TTTTAAAGTTGACCGTGTTTTTAAATCACTCTGGAGAAAAAGAAAAATTAATCAATA	2106
QY	1680	ATTAAACGGTGAATACAGGCTACTATACCTTGTCTCCAGATTAGCAGTTCTGTCTTT	1739
Db	2107	ATTAAACGGTGAATACAGGCTACTATACCTTGTCTCCAGATTAGCAGTTCTGTCTTT	2166
QY	1740	TCTTGCTTTAATGTGTAAGTGCAGAAAGACACCTCTGTGATTGTACGTGTCTACTGCA	1799
Db	2167	TCTTGCTTTAATGTGTAAGTGCAGAAAGACACCTCTGTGATTGTACGTGTCTACTGCA	2226
QY	1800	AAATGTGTAATTTTTTTCTCAGCTGCCTAATGATGGAATTATGCTATATGATAAATG	1859
Db	2227	AAATGTGTAATTTTTTTCTCAGCTGCCTAATGATGGAATTATGCTATATGATAAATG	2286
QY	1860	CTGATGGAGACACACAAACCAATTTGTCTCAGTCCATTTTCTCTCAAAAGCTGG	1919
Db	2287	CTGATGGAGACACACAAACCAATTTGTCTCAGTCCATTTTCTCTCAAAAGCTGG	2346
QY	1920	AATGTGCATTTGATCAGTGGGAGATGTACCTGGACAGCCCATGAAAAAGATCAACAG	1979
Db	2347	AATGTGCATTTGATCAGTGGGAGATGTACCTGGACAGCCCATGAAAAAGATCAACAG	2406
QY	1980	TTCCACCCCAAGGAGCCCTAATTTTTCTTAATTTTCAATTTAGGCTTCTAATGCTCTC	2039
Db	2407	TTCCACCCCAAGGAGCCCTAATTTTTCTTAATTTTCAATTTAGGCTTCTAATGCTCTC	2466
QY	2040	TTTCATCTCTGCTCTCTACGAGTTTACAGCTTTTCTGTTCATATGTAACTCACAT	2099
Db	2467	TTTCATCTCTGCTCTCTACGAGTTTACAGCTTTTCTGTTCATATGTAACTCACAT	2526
QY	2100	ACACCTCATTTTTCTCTCATCAACAACCCCAAGTACCCCAATGTCCTACCTTGATTA	2159
Db	2527	ACACCTCATTTTTCTCTCATCAACAACCCCAAGTACCCCAATGTCCTACCTTGATTA	2586
QY	2160	AGTAAAGAGGCTCTGCAATTAAGGGCTTGTCCAAGCAACGACGTGAGAGCGCTAGAC	2219
Db	2587	AGTAAAGAGGCTCTGCAATTAAGGGCTTGTCCAAGCAACGACGTGAGAGCGCTAGAC	2646
QY	2220	TGGCTCCATTTCCATCTCTATTTCTCAGCATTTGACATACCCAGAACCCCAATGTGGG	2279
Db	2647	TGGCTCCATTTCCATCTCTATTTCTCAGCATTTGACATACCCAGAACCCCAATGTGGG	2706
QY	2280	GCCCTCAGTATTCGATCAATTTATTTCTATTAAGAAGCAAAACAATCCCGCATTTGGCCCC	2339
Db	2707	GCCCTCAGTATTCGATCAATTTATTTCTATTAAGAAGCAAAACAATCCCGCATTTGGCCCC	2766
QY	2340	AGTTATTTAAGCATTTCTCAGATTTTACCTTGAAGAAATGCCATGCGGCTGTATTTCAAT	2399
Db	2767	AGTTATTTAAGCATTTCTCAGATTTTACCTTGAAGAAATGCCATGCGGCTGTATTTCAAT	2826
QY	2400	CTTCAACCTTGTCCTCTCTCTCTGAAGAAAGGAAAGTCAATGTGATATGCCCTGAGAAC	2459
Db	2827	CTTCAACCTTGTCCTCTCTCTCTGAAGAAAGGAAAGTCAATGTGATATGCCCTGAGAAC	2886
QY	2460	TAGTGCATGGCTTAACTGTCTCTTCCATGACTCTGCTTATCTGTTTCTATTTTTCTCTC	2519
Db	2887	TAGTGCATGGCTTAACTGTCTCTTCCATGACTCTGCTTATCTGTTTCTATTTTTCTCTC	2946
QY	2520	TTTTTCCACCGAAGTCTATATCTCAAGAAAGAGGACCTGGCCTTAAAGGCTCCTGGGCT	2579
Db	2947	TTTTTCCACCGAAGTCTATATCTCAAGAAAGAGGACCTGGCCTTAAAGGCTCCTGGGCT	3006
QY	2580	AAGAAATATCAAGTCCAGTGAAGAAATCCATTTGACTGACCCCTCTGCTTACCCCTTTGT	2639
Db	3007	AAGAAATATCAAGTCCAGTGAAGAAATCCATTTGACTGACCCCTCTGCTTACCCCTTTGT	3066
QY	2640	GATGAGAAAGCTCCCAAGGGGTTTGTCTTTTGACATTTACAGGCTTAACTCAGATCACCC	2699
Db	3067	GATGAGAAAGCTCCCAAGGGGTTTGTCTTTTGACATTTACAGGCTTAACTCAGATCACCC	3126

OY	2700	AGGGGCAAGAAAGAAAGTAACCTAAACCTAAACGCTCTTAATATGTAATTAATGTAAT	2759
Db	3127	AGGGGCAAGAAAGAAAGTAACCTAAACCTAAACGCTCTTAATATGTAATTAATGTAAT	3186
OY	2760	AGTTAATTAACGTGATTTGTAACATGCTGTACAGACAAATGTGATTTTTTTCACAGCTGC	2819
Db	3187	AGTTAATTAACGTGATTTGTAACATGCTGTACAGACAAATGTGATTTTTTTCACAGCTGC	3246
OY	2820	TGTGATTTGATTAATGCCATTTGGAATAGATGCTGTAAAGACAACAAGCCAGGTTCC	2879
Db	3247	TGTGATTTGATTAATGCCATTTGGAATAGATGCTGTAAAGACAACAAGCCAGGTTCC	3306
OY	2880	CTCAAGTCCCGTAGCAAAATTTTTCAAAAGTTAAATTTAAATTCATCTGTAATCTAG	2939
Db	3307	CTCAAGTCCCGTAGCAAAATTTTTCAAAAGTTAAATTTAAATTCATCTGTAATCTAG	3366
OY	2940	TGACAGAGAAATGGAACATGATAGAGACTTAAGATCTAGCCCAATTTTTATATTTACTT	2999
Db	3367	TGACAGAGAAATGGAACATGATAGAGACTTAAGATCTAGCCCAATTTTTATATTTACTT	3426
OY	3000	GTTAAGAGATTTTGAACAATTAATCTAAATTTCTTCAAGTTCAATTTCCCAATTAATCTAT	3059
Db	3427	GTTAAGAGATTTTGAACAATTAATCTAAATTTCTTCAAGTTCAATTTCCCAATTAATCTAT	3486
OY	3060	AATGATATGCTCATCATTTATAGGGCCCTGGAGAGCATTAATCTTGTAATGTAAATAT	3119
Db	3487	AATGATATGCTCATCATTTATAGGGCCCTGGAGAGCATTAATCTTGTAATGTAAATAT	3546
OY	3120	CATTGTTATTAATTAATTAATACATATTTGGCTTTTAAAGATTAAGATTTTAAAGATAT	3179
Db	3547	CATTGTTATTAATTAATTAATACATATTTGGCTTTTAAAGATTAAGATTTTAAAGATAT	3606
OY	3180	GTAACCTGTAAAAACATAAAAATGCAAAATGCGGTAAAGACAGTGTATTAATATGATTA	3239
Db	3607	GTAACCTGTAAAAACATAAAAATGCAAAATGCGGTAAAGACAGTGTATTAATATGATTA	3666
OY	3240	TTATATTTGTTATCATTAATCTAGCCGTGTTTTTTCCTGTGTGTATTTCTTCCCTTAAATGC	3299
Db	3667	TTATATTTGTTATCATTAATCTAGCCGTGTTTTTTCCTGTGTGTATTTCTTCCCTTAAATGC	3726
OY	3300	TTACAGAAATCTGTATCCCATTTCTTCAACACACCCGACAAACATTTCTGCTTTTTC	3359
Db	3727	TTTACAGAAATCTGTATCCCATTTCTTCAACACACCCGACAAACATTTCTGCTTTTTC	3786
OY	3360	CATGCC-GGTCATGCTAACTTTGAAGACTTCAAGCTCTTGCTTCCTCAATCCCTCTGCTG	3418
Db	3787	CATGCCGGGTCATGCTAACTTTGAAGACTTCAAGCTCTTGCTTCCTCAATCCCTCTGCTG	3846
OY	3419	GCACTCTGTATATGCTCTTTGAAATTAATTAATTAAGATCCCTAGGCTGCTATCAACATG	3478
Db	3847	GCACTCTGTATATGCTCTTTGAAATTAATTAATTAAGATCCCTAGGCTGCTATCAACATG	3906
OY	3479	GGCATCTTTGTGAGTACATGAATTAATCACTGCTGTGTTTTTACGAAGATGATTAATGC	3538
Db	3907	GGCATCTTTGTGAGTACATGAATTAATCACTGCTGTGTTTTTACGAAGATGATTAATGC	3966
OY	3539	TTTCAATGTGGATTTGATTTTTTCTTCTTCAATCAACAGAGGAAGTGA	3586
Db	3967	TTTCAATGTGGATTTGATTTTTTCTTCTTCAATCAACAGAGGAAGTGA	4014

XX	RESULT 4
ABL32337/C	
ID	ABL32337 standard; DNA, 7201 BP.
XX	
AC	
XX	ABL32337;
DT	
XX	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 310.
XX	
XX	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiartherosclerotic; antianemic; cytosolic; nontropic;

Qy	1441	GA	CTCGGAGGACCTCGAGTGTCTTCGAGCGTGAACCTCAGGCTCAAAAGCTCAACAG	1500
Db	2885	GA	TTTGGAGGATTTGTATGTTTTTTTGGATTTGGAAATTTAGTGTAAAGTTAAAGTTAAAGC	2944
Qy	1501	CAG	CCCTGAAACCCCAACCAAAAGGTTCTATGAGTTTATCATCTGCATCATGTGATTTTA	1560
Db	2945	TAG	TTTGAATTTAAATTAATTAAGGTTTATAGTTTATATTTGATATTCGATTAATCTGATTTTA	3004
Qy	1561	TAGA	ATPAACAACATGAATTTAAAGACATACCTCAACTGACCAAACTTAAGTAATTTT	1620
Db	3005	TAGA	ATPAATATATGAATTTAAAGATATTAATTTTAAATTCGATTAATTTTAAGTAATTTT	3064
Qy	1621	TTT	TAAAGTTTAAACCTGTCTTTTAAATCACTCTTGAGAAAAGAAAATTAATTAACAATTA	1680
Db	3065	TTT	TAAAGTTGATTTGATTTGTTTTTAAATATATTTTGGAGAAAAGAAAATTAATTAATTA	3124
Qy	1681	TTA	ACGGGATTAACAGGCTACTATACCTTGTCTCCAGATTTAGACAGTTCGTCTCTTT	1740
Db	3125	TTT	AACGGGATTAACAGGCTACTATATATATTTTGTGTTTAAATTTAGATGTTTGTGTTTTT	3184
Qy	1741	CTT	CCCTTAAAGTCGTAAGTCAGAGAGACACTCTGATATGTACAGTGTGTAACGCA	1800
Db	3185	TTT	GTGTTTAAAGTGTGAAGTGTGAAGAGATTTTGTGATGTGACGTGTATATGAATTA	3244
Qy	1801	AAT	GTATTTTTTTTTCTCAGCTGCTATGATGGATATGCTATTTATGAATTAAGATGC	1860
Db	3245	AAT	GTATTTTTTTTTTAACTGTATGATGGATGGATATGCTATTTATGAATTAAGATGT	3304
Qy	1861	TGA	TGGAGGACACACAAACCATTTGTTCCACAGCCATTTTCCCTCAAAACCTGGA	1920
Db	3305	TGA	TGGAGGAGTATATATTAATATATTTGTTTTTATGTTATTTTTTTTTTAAAGTTTGA	3364
Qy	1921	ATG	TGCCATTTGATCAGTGGAGAGATGATCTGGAACGACCCATGAAAGAGATCAACAGT	1980
Db	3365	ATG	TGTATTTATATATATGAGGAGATGATTTGATATGATTTATGAAAGATTAATATAGT	3424
Qy	1981	TCC	ACCCAGGAGCCCTATATTTTCTTAATTTCAATTTGAATGGCTCTAATTTGTCCTTT	2040
Db	3425	TTT	ATTTAAAGGATTTATATTTTTTTTAAATTTTAAATTTGAATTTGTTTTTAAATTTGTTTTT	3484
Qy	2041	TTT	CATTTCTGCTTCCTACAGTTTAAAGCTTTTTCGTGTTCAAAATGTGAATCAACATA	2100
Db	3485	TTT	ATTTTGTGTTTTTATTTAGTGTATATGTTTTTGTGTTTTTAATATGAAATTTATATA	3544
Qy	2101	CAC	CTCATTTTTTCCATCACAACCCCAAGNACCCAAAGTGCCTCATTCGATATTA	2160
Db	3545	TAT	TTTATATTTTTTTTATATATTAATTTTAAAGTATTAAGTGTTTTATTTTCGATATTA	3604
Qy	2161	GTA	AAGAGGCTCTGCTATTAAAGGCTTGTCCAAAGCAGCAGCTGAGAGCGCTAGAGCT	2220
Db	3605	GTA	AAGAGGCTTTTGTATTAAGGCTTGTTAAGGTAAGTATGAGAGGCGTTAGAGAT	3664
Qy	2221	GGC	TTCATTTTCATCTATTTCTCATCTGACTTTTGAATACCAAGAACCCCAACATGTGGGG	2280
Db	3665	GAT	TTTATTTTATTTTATTTTATTTTATGATTTTGAATTTTAAATTAATATGTGGGG	3724
Qy	2281	CCT	CAGATTTGATGATATTAATTTCTATTTAAAGAGCAAAACAATTTCCCGCATGTGCCCA	2340
Db	3725	TTT	ATTAAGTATTCATTAATTTATTTTATTAAGAGTAAATATATTTTCTGATGTGTTTA	3784
Qy	2341	GTT	ATTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCTGTATATTCACATCT	2400
Db	3785	GTT	ATTAAGTATTTTATTTTATTTATTTTGAAGAAATGTTATTCGGTTTGTATTTATTAAT	3844
Qy	2401	TTT	CACCTTGTCTCTTCCCTGAGAAAGAGAAAGTCAATTGATGCCCTCTGAGAACT	2460
Db	3845	TTT	ATTTTGTGTTTTTTTTTTTAAAGAGAGAAAGTATGTTGAGATGTTTTTGAAGAACT	3904
Qy	2461	AGT	GATAGGCTTAACATGTCCTTCCATGACTCCTGCTATATCTGTTTCTATTTCTCTCT	2520
Db	3905	AGT	GATAGGCTTAAATGTTTTTTTATTAAGATTTTGTATATTTGTTTTTATTTTTTTTTT	3964

Oy	2521	TTTCACCGAAGCTAAATCTCAAGAAAGCAGGCGCTGGCCTAGGGCTCAGGCTA	2580
Db	3365	TTTTATCGAAGTTATATATTTAAGAAAGTAGATATGGTTTAGGGTTTTGGTTA	4024
Oy	2581	AGAAATATCAAGTCACATGAGAAATCCCATGATGACCCCTCGCTTAACCCCTTGTG	2640
Db	4025	AGAAATATTAAGTTATAGTGAATAATTTATATGATGATTTTTTGTATATTTTTTGTG	4084
Oy	2641	ATGAGGAAGCTCCAGGGGTTTGCTTTTGCATGTATCAAGGCTACTCAGATCAACA	2700
Db	4085	ATGAGGAAGTTTTTAGGGGTTTTGTTTTTGTATGTATTTAGGTTAATTAAGTATATTA	4144
Oy	2701	GGGGCAAGAAAGGAAGTAAACCTAACTAATGCTGTAAATGTAAATATATGTATATA	2760
Db	4145	GGGGTAAAGAAAGGAAGTAAATTAATTAATATGTGTATTAATGTAAATATGTATAA	4204
Oy	2761	GTTAATTAAGTGTGATTTGACATGTGTACAGACAAATGTATTTTTTCAAGCTGCT	2820
Db	4205	GTTAATTAATGTGATTTGTATATGTGTATAGATTAATATGTATTTTTTATATGTGT	4264
Oy	2821	GTGATTTGATTAATGCAATTTGGATTAAGATATGCTGTAAAGACACAAAGCCAGTTCC	2880
Db	4265	GTGATTTGATTAATGATTAATTTGGAATAGATATGTTAAGATATTAAGTTAGTTT	4324
Oy	2881	TCAAGTCCGTAAGCAATTTTCAAAAGTAAATTTAATAATCACTAATTTGAATCTAGT	2940
Db	4325	TTAAGTTCTGATGAATATTTTTTAAAGTTAAATTTAAATATTAATTTGAATTTAGT	4384
Oy	2941	GACAGGAAGAAATGACATGATAGACTAAGATCTAGCCAAATTTATATTAATTCCTG	3000
Db	4385	GATAGGAAGAAATGATATGATAGATTAAGATTTAGTTTAAATTTATATTTATTTTGG	4444
Oy	3001	TTAGAGATTTTGAACAAATTAATCAAAATTTCTTCAAGGTTCAATTTCCCATTAACATA	3060
Db	4445	TTAGAGATTTTGAATTAATTAATTAATTTTAAAGTTAATTTTATATTAATATA	4504
Oy	3061	ATGATATCTCATTAATATAGGGGCCCTGGAGAGCATTAATTAATCTGTATATGTATATC	3120
Db	4505	ATGATATGTTAATTAATATAGGGGTTTGGAGAGTAAATTAATTTGTATATGTATATAT	4564
Oy	3121	ATGTGTATATTAATTAATCAATTTTGTCTTAAATCGATTAAGATTTTAAAGTATATG	3180
Db	4565	ATGTGTATATTAATTAATTAATATTTTGTTTTAAATGATTAAGATTTTAAAGTATATG	4624
Oy	3181	TAACTGTAAACATTAATATGCAAAATGCGGTAGAGAGACAGTATTAATTAATATATAT	3240
Db	4625	TAAATTTGAATTAATTAATATGTAATATGTGTAAAGATATGTATATTAATATATATAT	4684
Oy	3241	TATATGTATCAATTAATCAAGCTGTTTTTCTGTGTGTATTTCTCTTTAAATGCT	3300
Db	4685	TATATGTATATTAATTAATTTGTTTTTGTTTTTTGTGTATTTTTTTTTTAAATGTT	4744
Oy	3301	TACAGAAATCTGATATCCCATCTTGACACACACCCACAACATTTCTGCTCTTTTCC	3360
Db	4745	TTTGAATTTGTATTTTAAATTTTTTATTTATTTATTAATTAATTTTGTTTTTTTTTT	4804
Oy	3361	ATG-CCGTCATCTAATCTTGAAGCTGAGCTCTTCTCTCTCAATCCTCTCCGG	3419
Db	4805	ATGTCGGGTATATTAATTTGAAAGTTAGTTTTTTTTTTTTTAAATTTTTTTTTTGG	4864
Oy	3420	CACCTGTATATGCTTTTGAATTTCAATGTAAAGATCCCTAGCTGTATCAATGTG	3479
Db	4865	TATTTTGAATATGTTTTTGAATTTAATTAAGATTTTTTAGTGTTATATATATATG	4924
Oy	3480	GCATCTTTGTAGATCAATGAATTAATCAATGTGTGTGTTTACGAAGATGATTAAGCT	3539
Db	4925	GTAATTTTGTGATATATGAATTAATTAATTAATGTGTGTATTAAGAGATATATGTT	4984
Oy	3540	TCAATTTGGATTTGATTTTTCTCTCTCTATCAAGAGGAAGTGA	3586
Db	4985	TTATTTGGATTTGATTTTTTTTTTTTTTATATAGGAGAAAGTGA 5031	

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RESULT 6
AAT85162
ID AAT85162 standard; cDNA, 1915 BP.
XX
AC AAT85162;
XX
DT 14-DEC-1997 (first entry)
XX
DE Human chemokine receptor 88-2B cDNA.
XX
KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis; tumour;
KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW diagnosis; leukocyte trafficking; G protein coupled receptor; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 362..1429
FT /tag= a
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX MPI: 1997-341689/31.
XX
XX P-PSDB; AAM27124.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 7; Page 48-50; 65pp; English.
XX
XX This sequence comprises a full-length cDNA coding for novel human
XX chemokine receptor 88-2B (AAM27124), a G protein coupled receptor that is
XX involved in leukocyte trafficking. The 88-2B cDNA was obtained from a
XX macrophage cDNA library using 88-2B-specific primers. A full-length clone
XX (see AAT89161) for chemokine receptor 88C (AAM27123) was also obtained.
XX 88C and 88-2B cDNAs can be used to produce recombinant polypeptides in
XX transformed host cells for use in the treatment of e.g. atherosclerosis,
XX rheumatoid arthritis, tumours, asthma, viral infection, AIDS and
XX inflammatory conditions. Nucleic acid fragments can be used to isolate
XX genomic sequences, to detect alleles of the gene (for diagnosis or in
XX gene therapy), to alter receptor genetics to facilitate identification of
XX modulators and to produce knockout animals, and (antisense forms) to
XX alter/study the genetics and expression of the receptor
XX
XX Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;
XX
Query Match 9.6%; Score 344.2; DB 2; Length 1915;
Best Local Similarity 98.9%; Pred. No. 1.5e-64;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
XX
QY 3227 AATAATATGATTTATATGTTATGATATCATGAGCTGTTTTCCTGTGTGTAATTC 3286
DB 1 AATAATATGATTTATATGTTATGATATCATGAGCTGTTTTCCTGTGTGTAATTC 60
XX
QY 3287 TTCCCTTAAATGCTTACAGAAATCTGTATCCCATCTTTCACACCAACCCACACATTT 3346
DB 61 TTCCCTTAAATGCTTACAGAAATCTGTATCCCATCTTTCACACCAACCCACACATTT 120
XX
QY 3347 CTGCTCTTTTCCCAAGCC-GGTGATGCTTAAGCTTTGAAAGCTTCAAGTCTTTCTTCCTC 3405
DB 121 CTGCTCTTTTCCCAAGCCGGGTGATGCTTAAGCTTTGAAAGCTTCAAGTCTTTCTTCCTC 180

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QY 3406 AATCCTTCTCTGAGCAGCTGTGATATGCTTTTGAAATTCATGTTAAAGATCCCTAGGC 3465
DB 181 AATCCTTCTCTGAGCAGCTGTGATATGCTTTTGAAATTCATGTTAAAGATCCCTAGGC 240
XX
QY 3466 TGCTATCAATGTGGACATCTTTGTTGAGTACATGAATTAATCAACTGGTGTGTTTACGA 3525
DB 241 TGTATCAATGTGGACATCTTTGTTGAGTACATGAATTAATCAACTGGTGTGTTTACGA 300
XX
QY 3526 AGATGATTAATGCTTCATTTGAGGATTTGATTAATTTTCTTCTATCAGAGGAGAAATGA 3585
DB 301 AGATGATTAATGCTTCATTTGAGGATTTGATTAATTTTCTTCTATCAGAGGAGAAATGA 360
XX
QY 3586 A 3586
DB 361 A 361
XX
RESULT 7
ADC03342
ID ADC03342 standard; cDNA, 1915 BP.
XX
XX ADC03342;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human cDNA encoding chemokine receptor 88-2B.
XX
XX ss; gene; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
XX chemokine receptor; envelope protein; atherosclerosis;
XX Rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
XX AIDS; inflammatory condition; chromosome 3p21.
XX
XX Homo sapiens.
XX
XX
XX FH Key Location/Qualifiers
XX FT CDS 362..1429
XX FT /tag= a
XX FT /product= "Chemokine receptor 88-C"
XX FT /note= "This CDS, minus the STOP codon, is specifically
XX claimed in claim 11"
XX
XX US2002150888-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002US-00106623.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX 20-DEC-1996; 96US-00771276.
XX
XX (GRAY/) GRAY P W.
XX PA (SCHW/) SCHWEICKART V L.
XX PA (RAPO/) RAPORT C J.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX MPI: 2003-182491/18.
XX
XX P-PSDB; ADC03343.
XX
XX Screening for a modulator of HIV and SIV infection utilizing
XX polynucleotides that encode the 88C or 88-2B chemokine receptors, useful
XX for diagnosing and treating disorders such as atherosclerosis, arthritis,
XX AIDS and asthma.
XX
XX Claim 11; Page 18-20; 29pp; English.
XX
XX The invention relates to screening for a modulator of human
XX immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
XX infection, comprising contacting a first composition having an human
XX (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with
XX a second composition having an HIV or SIV envelope protein in the

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CC presence or absence of a compound. Also included are screening for a
 CC modulator of HIV infection, detecting HIV infection of cells (comprising
 CC contacting a cell that has been recombinantly modified to express at
 CC least one of human chemokine receptors 88C and 88-2B with HIV, and
 CC detecting HIV infection in the cell) and inhibiting HIV infection of
 CC cells (comprising contacting cells with an antibody to at least one of
 CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
 CC infection of the cell after the contacting step). The methods and
 CC compositions of the present invention are useful for the diagnosis and
 CC treatment of disorders associated with the aberrant expression or
 CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
 CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
 CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
 CC 2B are located on chromosome 3p21. The present sequence encodes human
 CC chemokine receptor 88-2B.

XX Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 9.6%; Score 344.2; DB 10; Length 1915;

Best Local Similarity 98.9%; Pred. No. 1.5e-64; Mismatches 3; Indels 1; Gaps 1;

Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAAATGATTAATTAATTTGATATCTAGGCTGTTTCTGTTGATATTC 3286
 DB 1 AATAATGATTAATTAATTTGATATCTAGGCTGTTTCTGTTGATATTC 60
 QY 3287 TTCCTTAAGCTTACAGAAATCTGTATCCCATCTTACACACCCCAACATTT 3346
 DB 61 TTCCTTAAGCTTACAGAAATCTGTATCCCATCTTACACACCCCAACATTT 120
 QY 3347 CTGCTTCTTTCCAGAGCC-GGTCAATGCTAATCTTGAAGCTTCTTCTCTTC 3405
 DB 121 CTGCTTCTTTCCAGAGCCGGGTCAATGCTAATCTTGAAGCTTCTTCTCTTC 180
 QY 3406 AATCTTCTCTGCGACCTCTGATATGCTTTGAATTCATGTTAAGATCCTTAGCC 3465
 DB 181 AATCTTCTCTGCGACCTCTGATATGCTTTGAATTCATGTTAAGATCCTTAGCC 240
 QY 3466 TGCCTATCAGTGGCATCTTTGTAGTACATGAATTAATCACTGGTGTATACGA 3525
 DB 241 TGCCTATCAGTGGCATCTTTGTAGTACATGAATTAATCACTGGTGTATACGA 300
 QY 3526 AGGATGATTAATCTTCAATTTGGGGAATTTCTTCTCTATCAGAGGAGAATGA 3585
 DB 301 AGGATGATTAATCTTCAATTTGGGGAATTTCTTCTCTATCAGAGGAGAATGA 360
 QY 3586 A 3586
 DB 361 A 361
 RESULT 8
 ID ADT90848 standard; cDNA; 1915 BP.
 XX ADT90848;
 AC ADT90848;
 XX 16-DEC-2004 (first entry)
 DT Human chemokine receptor 88-2B cDNA.
 DE Human chemokine receptor 88-2B cDNA.
 XX Chemokine receptor 88C; chemokine receptor 88-2B;
 KW human immunodeficiency virus; simian immunodeficiency virus; HIV; SIV;
 KW infection; vaccine; virucide; gene; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..361
 FT /tag= a
 FT CDS 362..1429
 FT /tag= c
 FT /product= "Human chemokine receptor 88-2B protein"

FT misc_feature 362..469
 FT /tag= b
 FT /note= "Encodes extracellular domain"
 FT misc_feature 539..574
 FT /tag= d
 FT /note= "Encodes extracellular domain"
 FT misc_feature 638..682
 FT /tag= e
 FT /note= "Encodes intracellular domain"
 FT misc_feature 752..814
 FT /tag= f
 FT /note= "Encodes intracellular domain"
 FT misc_feature 872..949
 FT /tag= g
 FT /note= "Encodes extracellular domain"
 FT misc_feature 1016..1081
 FT /tag= h
 FT /note= "Encodes extracellular domain"
 FT misc_feature 1148..1213
 FT /tag= i
 FT /note= "Encodes intracellular domain"
 FT misc_feature 1277..1426
 FT /tag= j
 FT /note= "Encodes intracellular domain"
 FT 3'UTR 1430..1915
 FT /tag= k
 PN US6797811-B1.
 PD 28-SEP-2004.
 XX 20-DEC-1996; 96US-00771276.
 XX 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX (ICOS-) ICOS CORP.
 PA Gray PW, Schweickart VL, Raport CJ;
 PI WPI; 2004-687775/67.
 DR P-PSDB; ADT90849.
 XX
 PT New antibodies specifically binding to (the extracellular domain of) a
 PT chemokine receptor 88C polypeptide expressed on the surface of cells,
 PT useful for inhibiting human or simian human immunodeficiency infection of
 PT such cells.
 XX
 XX Example 2; SEQ ID NO 3; 29pp; English.
 PS
 XX The invention relates to a novel antibody that specifically binds to the
 CC extracellular domain of a chemokine receptor 88C or 88-2B polypeptide
 CC expressed on the surface of cells. The antibody fails to cross-react with
 CC an MCP-1 receptor (CCR2-2) and is useful for inhibiting human or simian
 CC immunodeficiency virus (HIV or SIV) infection of the cells expressing
 CC chemokine receptor 88C or 88-2B. The invention is also used to detect 88C
 CC or 88-2B gene products their analogues or biologically active fragments.
 CC The antibody products may be used to as modulators of receptor activities
 CC or to diagnose tissue-specific variations in expression of 88-2B or 88C.
 CC The invention is also used in the preparation of vaccines. The present
 CC sequence is the human chemokine receptor 88-2B cDNA.
 XX
 SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;
 Query Match 9.6%; Score 344.2; DB 13; Length 1915;
 Best Local Similarity 98.9%; Pred. No. 1.5e-64; Mismatches 3; Indels 1; Gaps 1;
 Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 3227 ATAAATGATTAATTAATTTGATATCTAGGCTGTTTCTGTTGATATTC 3286
 DB 1 AATAATGATTAATTAATTTGATATCTAGGCTGTTTCTGTTGATATTC 60
 QY 3287 TTCCTTAAGCTTACAGAAATCTGTATCCCATCTTACACACCCCAACATTT 3346


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DB      61  TTCCTTAATGCTTTCAGAAATCTGTAATCCCATCTTCACACACACCCCAACATTT 120
OY      3347  CTGCTCTTTTCCCATNGCC-GGTCATNGCTAATCTTGAAGCTTCAAGCTTCTTCCG 3405
DB      121  CTGCTCTTTTCCCATNGCCGGGTCAATGCTAATCTTGAAGCTTCAAGCTTCTTCCG 180
OY      3406  AATCCTTCTCTCCGACCTCTGATATGCTTTGAAATTCATGATTAAGAAATCCCTAGGC 3465
DB      181  AATCCTTTTCCGACCTCTGATATGCTTTGAAATTCATGATTAAGAAATCCCTAGGC 240
OY      3466  TGCATATCATGTGGCATCTTTGTTGAGTACATGAAATTAATCACTGGTGTGTTTACGA 3525
DB      241  TGCATATCATGTGGCATCTTTGTTGAGTACATGAAATTAATCACTGGTGTGTTTACGA 300
OY      3526  AGGATGATTATGCTTCAATGNGGAGATGTAATTTTCTTCTCATACAGGAGAAATGA 3585
DB      301  AGGATGATTATGCTTCAATGNGGAGATGTAATTTTCTTCTCATACAGGAGAAATGA 360
OY      3586  A 3586
DB      361  A 361

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RESULT 9
ADU47727
ID ADU47727 standard; cDNA; 1915 BP.

ADU47727;

10-FEB-2005 (first entry)

Human chemokine receptor 88-2B cDNA.

Chemokine receptor; 88C; human immunodeficiency virus;
simian immunodeficiency virus; HIV; STIV; MCP-1; CCRK-2; 88-2B;
leukocyte trafficking; acquired immune deficiency syndrome; AIDS;
psoriasis; rheumatoid arthritis; atherosclerosis; tumour; asthma;
viral infection; inflammation; anti-HIV; virucide; antiproliferative;
antiarthritic; arteriosclerotic; anti-inflammatory; human; gene; ss.

Homo sapiens.

Location/Qualifiers

1..361

/*tag= a

362..1429

/*tag= b

/product= "Chemokine receptor 88-2B "

1430..1915

/*tag= c

US2004230037-A1.

18-NOV-2004.

04-FEB-2004; 2004US-00772037.

20-DEC-1995; 95US-00575967.

07-JUN-1996; 96US-00661393.

20-DEC-1996; 96US-00771276.

(ICOS-) ICOS CORP.

Gray PW, Schweickart VL, Raport CJ;

WPI; 2004-813308/80.

P-PSDB; ADU47728.

Modulating chemokine receptor 88C-mediated human or simian

immunodeficiency virus infection comprises administering an antibody that

binds to chemokines or a polypeptide comprising an antigen-binding

fragment of the antibody.

Example 2; SEQ ID NO 3; 28bp; English.
The invention relates to a method of modulating chemokine receptor 88C-mediated human or simian immunodeficiency virus (HIV or SIV) infection of cells. The method comprises administering to a mammalian subject a composition comprising an antibody or a polypeptide comprising an antigen-binding fragment of the antibody, where the mammalian subject is infected with HIV or SIV, and where the antibody is administered in an amount that modulates HIV or SIV infection of 88C-expressing cells in the subject. The antibody is a humanised antibody which specifically binds to the extracellular domain of the chemokine receptor 88C polypeptide and fails to cross-react with an MCP-1 receptor (CCRK-2) or binds to the N-terminal 20 amino acid peptide of the 88C receptor. The invention also provides purified and isolated nucleic acids encoding chemokine receptors, namely 88-2B and 88-C, involved in leukocyte trafficking. The modulators of the chemokine receptors of the invention are useful for treating diseases such as HIV or SIV infection (e.g. acquired immune deficiency syndrome (AIDS)), psoriasis, rheumatoid arthritis, atherosclerosis, tumour growth suppression, asthma, viral infection, or inflammation. The present sequence is the human chemokine receptor 88-2B cDNA.

Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 9.6%; Score 344.2; DB 13; Length 1915;
Best Local Similarity 98.9%; Pred. No. 1.5e-64;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

3227 ATAAATGATTATATATATGTTATCATATCTAGCCGTTTTCGTTGTAATTC 3286

1 ATAAATGATTATATATATGTTATCATATCTAGCCGTTTTCGTTGTAATTC 60

3287 TTCCTTAATGCTTACAGAAATCTGATATCCCATCTTTCACACACCCCAACATTT 3346

61 TTCCTTAATGCTTACAGAAATCTGATATCCCATCTTTCACACACCCCAACATTT 120

3347 CTGCTCTTTTCCCATNGCC-GGTCATNGCTAATCTTGAAGCTTCAAGCTTCTTCCG 3405

121 CTGCTCTTTTCCCATNGCCGGGTCAATGCTAATCTTGAAGCTTCAAGCTTCTTCCG 180

3406 AATCCTTCTCTCCGACCTCTGATATGCTTTTGAATTCATGATTAAGAAATCCCTAGGC 3465

181 AATCCTTCTCTCCGACCTCTGATATGCTTTTGAATTCATGATTAAGAAATCCCTAGGC 240

3466 TGCATATCATGTGGCATCTTTGTTGAGTACATGAAATTAATCACTGGTGTGTTTACGA 3525

241 TGCATATCATGTGGCATCTTTGTTGAGTACATGAAATTAATCACTGGTGTGTTTACGA 300

3526 AGGATGATTATGCTTCAATGNGGAGATGTAATTTTCTTCTCATACAGGAGAAATGA 3585

301 AGGATGATTATGCTTCAATGNGGAGATGTAATTTTCTTCTCATACAGGAGAAATGA 360

3586 A 3586

361 A 361

RESULT 10

ACN44478 standard; DNA; 54701 BP.

ACN44478;

18-NOV-2004 (first entry)

Human genomic sequence hCG24071.

Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

Homo sapiens.

WO2003073826-A2.

PF 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX MPI; 2003-328604/31.
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX
XX Claim 1; SEQ ID NO 622; Opp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
XX are associated with carcinomas. The sequences are useful for: (i) for
XX screening drug candidates; (ii) for screening of bioactive agent capable
XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX a bioactive agent capable of modulating the activity of CAP; (iv) for
XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
XX carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
XX (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
XX determining Carcinoma Associated (CA) gene copy number. In addition, the
XX CA genes are useful as DNA vaccines and the CAP are useful as markers of
XX carcinoma including lymphoma. The present sequence is one such CA coding
XX sequence. Note: This patent is an equivalent to basic patent
XX US2002182586A1, for which no sequence data was published
XX
XX Sequence 168821 BP; 39588 A; 43389 C; 45655 G; 40189 T; 0 U; 0 Other;
XX

Query Match 5.9%; Score 210.2; DB 11; Length 168821;
Best Local Similarity 75.6%; Pred. No. 8.6e-35;

Matches 288; Conservative 0; Mismatches 88; Indels 5; Gaps 2;

QY 1008 AGAATTCACCTTGATGAGACGCGGTAGACAGGTAAACCATATCAGGTTTAAATTT 1067
DB 166223 AGAATTCCTTCTCTATTTCTGATGATTAATTTGAACTCCATAGAAATCCTATTTAT 166282
QY 1068 TTAATTTTAAATTTAATTTAATTTAATTTTGAATGAGTCTGCTG--TCGCC 1125
DB 166283 TTA---TTTATTTAATTTAATTTAATTTAATTTTGAACGGTGTCTGCTATCACC 166339
QY 1126 CAGGCTGAGTGACGCGCGGTATACAGATTCACTGACGCTCAACTTCTAGGCTCAAG 1185
DB 166340 CAGGCTGAGTGACGCGCGGTATACAGATTCACTGACGCTCAACTTCTAGGCTCAAG 166399
QY 1186 GGAATTCCTCCACCTGACGCGCGGTATGAGTGGGACACACGATGCGCACCAAGCTG 1245
DB 166400 GGAATTCCTCCACCTGACGCGCGGTATGAGTGGGACACACGATGCGCACCAAGCTG 166459
QY 1246 GCTAATTTCTAATTTTGTAGAGATAGATCTCAATATTTGTCAGGCTGTCTTGA 1305
DB 166460 GCTAATTTCTAATTTTGTAGAGATAGATCTCAATATTTGTCAGGCTGTCTTGA 166519
QY 1306 ATTCTCGGCTCAGTGAGCTTCCACCTGCGCTCCCAAGTACTGGAGTTACAGGCAT 1365
DB 166520 ATTCTCGGCTCAGTGAGCTTCCACCTGCGCTCCCAAGTACTGGAGTTACAGGCAT 166579
QY 1366 GAGCCCAAGTCCCTGCGCCAT 1386
DB 166580 GAGCCCAAGTCCCTGCGCCAT 166600

RESULT 14
ABV76540/c
ID ABV76540 standard; cDNA; 1215 BP.
XX
XX ABV76540;
XX
XX 20-FEB-2003 (first entry)
XX

DE Human protein phosphatase 12.76-encoding cDNA.
XX
XX Human; protein phosphatase 12.76; recombinant production; gene therapy;
XX embryonic development disorder; tumour; cancer; cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 9..359
XX FT /tag= a
XX FT /product= "Human protein phosphatase 12.76"
XX
XX CN1358852-A.
XX
XX 17-JUL-2002.
XX
XX 13-DEC-2000; 2000CN-00127882.
XX
XX 13-DEC-2000; 2000CN-00127882.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX MPI; 2002-733573/80.
XX
XX P-PSDB; ABP58504.
XX
XX Novel polypeptide-human protein phosphatase 12.76 and polynucleotide for
XX encoding said polypeptide.
XX
XX Claim 6; Page 26-27 (Disclosure); 33pp; Chinese.
XX

CC The invention relates to human protein phosphatase 12.76 (ABP58504) and
CC nucleic acids encoding it (ABV76540). The protein has a molecular weight
CC of 12.76 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. Protein
CC phosphatase 12.76 can be used in the treatment of a variety of diseases
CC such as embryonic development disorders and tumours. The present sequence
CC represents cDNA encoding human protein phosphatase 12.76
XX

Sequence 1215 BP; 345 A; 276 C; 281 G; 313 T; 0 U; 0 Other;

Query Match 5.9%; Score 210; DB 6; Length 1215;

Best Local Similarity 76.3%; Pred. No. 1.9e-35;

Matches 258; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1064 TTTTAAATTTTAAATTTAATTTAATTTAATTTTGAATGAGTCTGCGTGTG 1123
DB 823 TTTTAAATTTTAAATTTAATTTAATTTAATTTTGAAGACAGGCTCACTGTCA 764
QY 1124 CCAGGCTGAGTGACGCGCGGTATACAGATTCACTGACGCTCAACTTCTAGGCTCA 1183
DB 763 CCAGGCTGAGTGACGCGCGGTATACAGATTCACTGACGCTCAACTTCTAGGCTCA 704
QY 1184 AGGATTCCTCCACCTGACGCGCGGTATGAGTGGGACACAGTATGCGCACCAATGCC 1243
DB 703 AGGATTCCTCCACCTGACGCGCGGTATGAGTGGGACACAGTATGCGCACCAATGCC 644
QY 1244 TGAGTAAATTTCTAATTTTGTAGAGATAGATCTCAATATTTGTCAGGCTGTCTT 1303
DB 643 TGAGTAAATTTCTAATTTTGTAGAGATAGATCTCAATATTTGTCAGGCTGTCTT 584
QY 1304 GAATTCCTGAGCTCAGTGAGCTTCCACCTGCGCTCCCAAGTACTGGAGTTACAGGC 1363
DB 583 CAATCTCTGAGCTCAGTGAGCTTCCACCTGCGCTCCCAAGTACTGGAGTTACAGGC 524
QY 1364 ATGAGCCCAAGTCCCTGCGCCATATGAGATTTCTGTC 1401
DB 523 GTGAGCCCAAGTCCCTGCGCCATATGAGATTTCTGTC 486

RESULT 15

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:41:27 ; Search time 17670.5 Seconds
(without alignment)
11535.651 Million cell updates/sec

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Perfect score: 3586
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_strs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3586	100.0	3586	AR164120	Sequence
2	3586	100.0	3586	BD128570	Rosinophi
3	3586	100.0	3586	AX030930	Sequence
4	3494.4	97.4	5791	AX705064	Sequence
5	3494.4	97.4	5791	AF247361	Sequence
6	3494.4	97.4	177334	AF247361	Homo sapi
7	3492.8	97.4	197279	AC138069	Homo sapi
8	3481.6	97.1	220865	AC104439	Homo sapi
9	3408.6	99.1	7010	HSR312688	Homo sapi
10	3388	94.5	3388	AF22449682	Homo sapi
11	2406	67.1	7201	AF237381	Homo sapi
12	2271.8	63.4	7201	AX345239	Sequence
13	1066.2	29.7	1310	AF262300	Homo sapi
14	358.6	10.0	436	AF262304	Homo sapi
15	344.2	9.6	1915	AKS84940	Sequence
16	344.2	9.6	1915	BD006761	Chemokine
17	344.2	9.6	1915	BD017703	Chemokine
18	308.8	8.6	167298	AP006436	Sus scrofa

19	219.8	6.1	112967	8	AC025177	Homo sapi
20	218.2	6.1	123551	8	AC026361	Homo sapi
21	218.2	6.1	131329	8	AC004873	Homo sapi
22	218.2	6.1	157435	8	HS50024	Human DNA
23	217.8	6.1	146740	8	CNS01DTX	Human chr
24	217	6.1	143060	8	AL329472	Human DNA
25	217	6.1	151846	8	AP001630	Human DNA
26	217	6.1	180236	14	AC020600	Homo sapi
27	217	6.1	255952	14	AL513473	Homo sapi
28	217	6.1	340000	8	AP001748	Homo sapi
29	216.8	6.0	148065	8	CNS086CF	Human chr
30	216.6	6.0	39282	8	AC005596	Homo sapi
31	215.6	6.0	120538	8	AC004815	Homo sapi
32	215.6	6.0	121496	8	AC093391	Homo sapi
33	215.2	6.0	45597	8	AP000533	Homo sapi
34	215	6.0	174913	8	AL158819	Human DNA
35	214.8	6.0	93426	8	AL359732	Human DNA
36	214.6	6.0	38468	8	U51560	Homo sapi
37	214.6	6.0	176343	8	CNS01DX3	Human chr
38	214.4	6.0	185376	8	AC005096	Homo sapi
39	213.6	5.9	56913	8	HS67C13	Human DNA
40	213.2	5.9	185353	8	AL162732	Human DNA
41	212.8	5.9	124950	8	AC108059	Homo sapi
42	212.8	5.9	136876	8	AC112499	Homo sapi
43	212.6	5.9	177957	14	AC025298	Homo sapi
44	212.6	5.9	37650	8	HSU131B10	Human DNA
45	212.6	5.9	123708	8	HS190A9	Homo sapi

ALIGNMENTS

RESULT 1	AR164120	3586 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	AR164120	Sequence 3 from patent US 6271347.			
DEFINITION	AR164120				
ACCESSION	AR164120.1	GI:16235066			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 3586)				
AUTHORS	Daugherty B.L., Demartino J.A., Siciliano S.J. and Springer M.S.				
TITLE	Rosinophi1 ectoxin receptor				
JOURNAL	Patent: US 6271347-A 3 07-AUG-2001;				
FEATURES	Location/Qualifiers				
source	1..3586				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 3586; DB 6; Length 3586;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 3586; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	GGATCCCTACCTTCCCTCCATCAGAGTGAAGGCGCTCTCTGTAAGATGGGA	60		
DB	1	GGATCCCTACCTTCCCTCCATCAGAGTGAAGGCGCTCTCTGTAAGATGGGA	60		
QY	61	CCCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACCAAGATGGGCGAGTGT	120		
DB	61	CCCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACCAAGATGGGCGAGTGT	120		
QY	121	AAATTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGAAGATTTCTGCTTT	180		
DB	121	AAATTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGAAGATTTCTGCTTT	180		
QY	181	GTTCATGCGAGGCGAGGAGTCAAGAGGCGAGGCTTGTCTGCTTACCAAGTGA	240		
DB	181	GTTCATGCGAGGCGAGGAGTCAAGAGGCGAGGCTTGTCTGCTTACCAAGTGA	240		
QY	241	GGAAAAAGTGCATACCTTGGGCGAGGCGCGCTGTGTGAGGCGTAGTGTAAACA	300		

|||||
Db 241 GGAAGGCTAGACCTGGGCGAAGGCCAGGGCCCTGGTGGAGGGCTAGTGTAAACA 300
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Qy 301 GAGGCTCTCCATTCACAGCCCAAGGAAGCTAAGATGAATACCTCAGATGATATTAGC 360
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Db 301 GAGGCTCTCCATTCACAGCCCAAGGAAGCTAAGATGAATACCTCAGATGATATTAGC 360
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Qy 361 TACAACCAACAAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAACAGAGTCAACCCCA 420
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Db 361 TACAACCAACAAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAACAGAGTCAACCCCA 420
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Qy 421 TCAGACAGACCAAGATCATTAATATCAAGACCAAGAGACAGAAACACCCCTTCCCA 480
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Db 421 TCAGACAGACCAAGATCATTAATATCAAGACCAAGAGACAGAAACACCCCTTCCCA 480
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Qy 481 CTCGCCCCAGTCCTCAAGTTGATGAGGCCCTTCCCGAGATCTCGCCACCATCTTGA 540
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Db 481 CTCGCCCCAGTCCTCAAGTTGATGAGGCCCTTCCCGAGATCTCGCCACCATCTTGA 540
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Db 841 GTTGAACCTCATTTGTAATCTTGGACAAGGGGCAATCCATATCTGCAAGAGATAG 840
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Qy 841 TTAACCAAGGTGAATGCTGCAAGAGAGATGGGGATTTTACTTTGTTTGTGCT 900
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Db 841 TTAACCAAGGTGAATGCTGCAAGAGAGATGGGGATTTTACTTTGTTTGTGCT 900
|||
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Qy 961 GGCATTTTGAAGGCTTAATTCAAACCTCTCACTATTTTGTATCTAAGATTCACCTTG 1020
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Db 961 GGCATTTTGAAGGCTTAATTCAAACCTCTCACTATTTTGTATCTAAGATTCACCTTG 1020
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Qy 1021 ATTTGAAGCTGGGTAAGCAAGGTAAACATATCAAGGTTTAAATTTTAAATTTTAA 1080
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Db 1021 ATTTGAAGCTGGGTAAGCAAGGTAAACATATCAAGGTTTAAATTTTAAATTTTAA 1080
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Qy 1141 CGGCGTATCAAGTTCACTGAGCTCAACCTTCTAAGGCTCAAGGATTCCTCCACCTC 1200
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Qy 1321 TGAAGCTCCCACTGGGCTCCCAAGTACTGGGATTTAAGGATGAGCCAGTCTCCCT 1380
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|||||
Db 1321 TGAAGCTCCCACTGGGCTCCCAAGTACTGGGATTTAAGGATGAGCCAAAGTCTCCCT 1380
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Qy 1381 GCCCATATAGATTTTCTGTCTATGATCCCATGACAGTATTAACAAGACTTGGCTGT 1440
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Qy 1441 GACTGTGAGAGCTGCAATGCTTTCTTGAAGCTGGAATTCAGTGTAAAGCTCATAG 1500
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QY 2641 ATGGAAGCTCCAGGGGTTTCTTTTTCAGTGAAGGAGCTTAACAGATCATCA
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QY 2701 GGGGCAAGAAAGAAAGTAACTAAATGCTGCTTAATATTTGTAATTA
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QY 2761 GTTAACTGCTGATTTGTAATGCTGTAACAGAAATGCTATTTTTCAGAGCTGCT
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QY 2821 GTGATTTGCTATGCTGCTTGAATTAAGATGCTGTAAGAGCAGAGCAGGTTCC
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QY 2881 TCAAGTCCCTAGCAAAATTTTTCAGAAAGTAAATTTAAATCACTACATTTGATCTAGT
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RESULT 2
BD128570 3586 bp DNA linear PAT 18-SEP-2002
LOCUS Bostnophil eotaxin receptor.
DEFINITION BD128570
ACCESSION BD128570.1 GI:23223515
VERSION JP 2002503950-A/2.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 3586)
AUTHORS Daugherty, B.L., Demartino, J.A., Springer, M.S. and Siciliano, S.J.
TITLES Bostnophil eotaxin receptor
JOURNAL Patent: JP 2002503950-A 2 05-FEB-2002;
MERCK & CO INC
COMMENT OS Unidentified
PN JP 2002503950-A/2
PD 05-FEB-2002
PF 24-APR-1997 JP 1997538970
PR 26-APR-1996 US 08/640991 26-APR-1996 US 60/016158 PR
17-JAN-1997 GB 9700894.0
PI BRUCE L DAUGHERTY, JULIE A DEMARTINO, MARTIN S SPRINGER PI
PC C07K14/705, C07K14/715, C12N15/12
CC Strandedness: Single;
CC Topology: Linear;
CC Bostnophil eotaxin receptor
FT Key location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No: 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2641	ATGGGAAGCTCCCAAGGGTTTGTCTTTTGCATGTTACAGAGCTTAATCAAGATCAACA	2700
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Db	3361	ATGCGCGTCAATCTTAACCTTTGAAGCTTCAAGCTCTTCTCTCAATCTCTCTCTGCG	3420
Qy	3421	ACCTCTGATATGCTTTTGAATTAATCAATGTTAAAGATTCCTAAGCTGTATCAACATGCG	3480
Db	3421	ACCTCTGATATGCTTTTGAATTAATCAATGTTAAAGATTCCTAAGCTGTATCAACATGCG	3480
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Db	3481	CATCTTTTGTAGTACATGAATAATCAATCACTGTGTGTGTTTACGAAGATGATTAATGCTT	3540
Qy	3541	CATTTGAGGATTTGATTTTTTCTTCTTCTATCAACAGGAGAAAGTGA 3586	
Db	3541	CATTTGAGGATTTGATTTTTTCTTCTTCTATCAACAGGAGAAAGTGA 3586	

RESULT 3			
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LOCUS	AX030930		
DEFINITION	Sequence 3 from Patent EP1012190.		
ACCESSION	AX030930		

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VERSION      AX030930.1  GI:10278335
KEYWORDS
SOURCE
ORGANISM
REFERENCE    1
AUTHORS      Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
TITLE        Eosinophil eotaxin receptor
JOURNAL      Patent: EP 1012190-A 3 28-JUN-2000;
              MERCK & CO INC (US)
FEATURES
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Quer

Best Local Similarity 100.0%; Pred. NOI 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGATCCCTACCTTCCCCATCAGAGCTAGGGGCAAGAGGCTCTCTGCTAAGATGGGA 80

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22

E 49

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QY	1021	ATTGAGACTGGGTATACAGATGTAAGAAACATATCAGTCTTTTAAATTTTAAATTTTAAAT	1080
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Db	1141	CGGCGTATTCACAGTTTCATCTGACAGCTTCAACTTTAGGCTTCAGAGATTTCTCCACCTC	1200
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Db	1201	AGCCCCCAAGATATGTGGGACCAACAGATGCGCCACATGCGCTGCTTATTTCTTATTT	1260
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Db	1261	TTTTGTAGATATGAGATCTCACTATATTTGTCCAGGCTGTCTGAAATTCCTGGGCTCAGG	1320
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Db	1381	GCCCATATGAGATTTTCTGTCTGTATCCCATGAGCTATAGTATCAAGAGACCTTGGCTGCT	1440
QY	1441	GACTCTGAGAGACCTGCAATGCTTTCTTGAGCTGTACATTCAGAGCTTAAAGCTCATATGG	1500
Db	1441	GACTCTGAGAGACCTGCAATGCTTTCTTGAGCTGTACATTCAGAGCTTAAAGCTCATATGG	1500
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Db	1501	CAGCCCTGAACCCCAAAACGTTCTATGTTTATCATCTGATCATGTGATTTTA	1560
QY	1561	TAGAATATAACATATAATTAAAGACATACCTTCAAACCTGAGCAAACTTAAAGTAAATTT	1620
Db	1561	TAGAATATAACATATAATTAAAGACATACCTTCAAACCTGAGCAAACTTAAAGTAAATTT	1620
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Db	1681	TTTAAACGATGTAACAGGCTACTATACTTTGTCTTCAGAAATTAACAGTTCGTCTTTT	1740
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Db	1741	CTTTCCTTATGATGCTGAAGTGCAGAAAGACATCTCTGTGATTTGTACGTGTATACAGAA	1800
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Db	1801	AATGTGTATTTTTTTCTCAGGCTGATATGGAATTGATATATGATTAATGAATTAAGATGC	1860
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Db	1861	TGATGGAGGACACACAAACCATTTGTTCTCGATCCATTTTCTCTCAAAAGCTGG	1920
Qy	1921	ATGTCGCAATGATCAGTGGAGATGACCTGGACAGACCCATGAAAAGATCACAAGT	1980
Db	1921	ATGTCGCAATGATCAGTGGAGATGACCTGGACAGACCCATGAAAAGATCACAAGT	1980
Qy	1981	TCGACCCGAAGGAGCCCTAATTTTCTCTAATTTCAATTGAAATGGCTCTAAATGTCCTCT	2040
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Db	2041	TTCAATCTCGCTCCACACAGTTTTCAGCTTTTTCGTGTTCAAAATGTGAACTCACAATA	2100
Qy	2101	CACCTCAATTTTCTCATCAAAACCCCAAGTGAACCAATGTCCTCACTTTGATATPAA	2160
Db	2101	CACCTCAATTTTCTCATCAAAACCCCAAGTGAACCAATGTCCTCACTTTGATATPAA	2160
Qy	2161	GTTAAAGGAGGCTCTGCATTTAAGGGCTGTCTCAAGGACGACGCTGAAGGCGTAGGACT	2220
Db	2161	GTTAAAGGAGGCTCTGCATTTAAGGGCTGTCTCAAGGACGACGCTGAAGGCGTAGGACT	2220
Qy	2221	GGCCTCAATTTCCATCTCTAATTCAGTCACTTTGACTACCCAGAAACCCCAAGTGTGGG	2280
Db	2221	GGCCTCAATTTCCATCTCTAATTCAGTCACTTTGACTACCCAGAAACCCCAAGTGTGGG	2280
Qy	2281	CCTCAGTATTCGATCAATATATTCTATTAAAGAGCAAAACAATCCCCGATTTGGCCCCA	2340
Db	2281	CCTCAGTATTCGATCAATATATTCTATTAAAGAGCAAAACAATCCCCGATTTGGCCCCA	2340
Qy	2341	GTTATTAAAGCATTTCTCAGATTTACCTTGAAGAAATGCCCATGGCCTGTATTTCAATC	2400
Db	2341	GTTATTAAAGCATTTCTCAGATTTACCTTGAAGAAATGCCCATGGCCTGTATTTCAATC	2400
Qy	2401	TTCAACCTGTGCCCCCTGCTCTGAGAAAGGAAAGTCAGTGGATGCGCTCTGAGAACT	2460
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Db	3607	GTAACCTGTAAAAACATAAATATGCAAAATATGCGTAAGACAGTAGTAATAATATGATTA	3666
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Qy	3300	TTACAGAAATCTGATATCCCATCTCTGACACACACCCACAAACATTCCTGCTCTTTCC	3359
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Qy	3360	CATGCC-AGTCATCTAATCTTTGAAAGCTTAGCTCTTCCCTCCATCTCTCTG	3418
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Qy	3419	GCACCTCTGATATGCTTTTGAAATATCATATGTTAAAGAAATCCCTAAGGCTCATCAATG	3478
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Qy	3419	GGCATCTTTGTGAGTACATGAAATAAATCACTGATGTGTTTTACGAAGATGATATATGC	3538
Db	3907	GGCATCTTTGTGAGTACATGAAATAAATCACTGATGTGTTTTACGAAGATGATATATGC	3966
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RESULT 5	AF247361	5791 bp	DNA	linear	PRI 26-JUN-2002
LOCUS	AF247361				
DEFINITION	Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.				
ACCESSION	AF247361				
VERSION	AF247361.1	GI:19110542			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 5791) Vilh,S., Dayhoff,D.B., Wang,C.B., Imam,Z., Ehrenberg,P.K. and Michael,N.L.				
TITLE	Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rate RATA-less Promoter Structure Conserved between Drosophila and Humans				
JOURNAL	Genomics 80 (1), 86-95 (2002)				
PUBMED	12079287				
REFERENCE	2 (bases 1 to 5791)				
AUTHORS	Vilh,S., Dayhoff,D.B., Wang,C.B., Ehrenberg,P.K. and Michael,N.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA				

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DB	433	GGATCCCTACCTTCCCATCAAGCTAGGGGGCATGAGCGCTCTCTGCTAAGATGGGGA	492
QY	61	CCCCAAGAAATGCTCCCTGTGGGGGCACTTCCCTTACAGATGGGAATGGCAGTGGGTT	120
DB	493	CCCCAAGAAATGCTCCCTGTGGGGGCACTTCCCTTACAGATGGGAATGGCAGTGGGTT	552
QY	121	AAGTTGTGTGTACGGCAGAAAAAAGATTTAGTTTGTACTCTTGAGAGTTCTCGGTTT	180
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Db	1687	TTTTTGTAGAGATAGAGATCTCATATATTTGTCACAGCTGGTCTGAAATTCGCGGCTCAG	1746
QY	1320	GTGACCTCCCACTGGGCTTCCCAAAGTACTGGATTAACAGCATGAGCCAAAGTCTCCC	1379
Db	1747	GTGACCTCCCACTGGGCTTCCCAAAGTACTGGATTAACAGCATGAGCCAAAGTCTCCC	1806
QY	1380	TGCCCATATGAGATTTTCTGTCTCTGATTCCTATGACGTATGAAATCAAGGACTTGGCTGC	1439
Db	1807	TGCCCATATGAGATTTTCTGTCTCTGATTCCTATGACGTATGAAATCAAGGACTTGGCTGC	1866
QY	1440	TGACTCTGAGGAGCTGCATGCTTCTTGAAGCTGTGAACCTTCAGTCTTAAAGCTCATAAG	1499
Db	1867	TGACTCTGAGGAGCTGCATGAGTCTTCTTGAAGCTGTGAACCTTCAGTCTTAAAGCTCATAAG	1926
QY	1500	GCAAGCCCTGAACCCCAACCAAAAGGTTCTATGTATTATCATCTGATCATGTGATTTT	1559
Db	1927	GCAAGCCCTGAACCCCAACCAAAAGGTTCTATGTATTATCATCTGATCATGTGATTTT	1986
QY	1560	ATGAGAAATPAACAATGAATTAAGACATACCTCACTAAGCAAACTTAAGTAATTT	1619
Db	1987	ATGAGAAATPAACAATGAATTAAGACATACCTCACTAAGCAAACTTAAGTAATTT	2046
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Db	2047	TTTTTAAAGTTTGAACCTGTTTTTTAATTCATCTTGGAGAAAAAGAAAAATTAATCAATA	2106
QY	1680	ATTAACCGGTGAATPAACGGCTACTATATCTTTGTCTCCAGAAATTAGCATTTCTGTTCTTT	1739
Db	2107	ATTAACCGGTGAATPAACGGCTACTATATCTTTGTCTCCAGAAATTAGCATTTCTGTTCTTT	2166

QY	1740	ICTGCTTTAAGTCTGAAGTGCAGGAAGACACTCTGTAAATGACGTGTGAATCTACAA	1799
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QY	1800	AAATGTGAATTTTTTTCTCAGCTGCTATGGAATTGATTAATGCTAATTAATTAAGATG	1859
Db	2227	AAATGTGAATTTTTTTCTCAGCTGCTATGGAATTGATTAATGCTAATTAATGAATGAATG	2286
QY	1860	CTGATGGAGACACACAAACCAATTTGTCTCAGTCCATTTTCTCTCAAAAGCTCG	1919
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QY	1980	TTCCACCAAGGAGCCCTAATTTTCTTAATTTCAATTGAATGGCTCTTAATTTCTCTC	2039
Db	2407	TTCCACCAAGGAGCCCTAATTTTCTTAATTTCAATTGAATGGCTCTTAATTTCTCTC	2466
QY	2040	TTTCAATTCCTGCTTCTACACAGTTTTCACAGTTTTCAGCTTTTCTGTTCAAATGTGAATCAAT	2099
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Db	2527	ACACTCTAATTTTCTCTATCAACAACCCCAAGTAACCAATGTGTCCTCATTTGCAATTA	2586
QY	2160	AGTAAAGAGGCTCTGCATTTAAGGGCTTGTCAAGGACGACGCTGAAGGCGCTAAGAC	2219
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QY	2220	TGGCTCAATTTCCACTCTATTTCTCACTGACTTTCACGACCCAGAACCCCAACGTGTGG	2279
Db	2647	TGGCTCAATTTCCACTCTATTTCTCACTGACTTTCACGACCCAGAACCCCAACGTGTGG	2706
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Db	2707	GCTCAGATTTTCGATCAATTTCTTATTTAABAGCAAAAAACAATTTCCCGGATGTGGCCC	2766
QY	2340	AGTTATTAAGCAATTTCTCAGATTTACCTGAGAAATGCCATGGGCGTGTATTTTCAAT	2399
Db	2767	AGTTATTAAGCAATTTCTCAGATTTACCTGAGAAATGCCATGGGCGTGTATTTTCAAT	2826
QY	2400	CTTCAACCCCTTGCTCTCTCTCTAAGAAAGAAAGTCAGTGTGATGCCCTGAGAGAAC	2459
Db	2827	CTTCAACCCCTTGCTCTCTCTCTAAGAAAGAAAGTCAGTGTGATGCCCTGAGAGAAC	2886
QY	2460	TAGTGCATGCTTAACTGTCTCTCTCAAGACTCTGCTCTTATCTGTTTCTATTTTCTCTCC	2519
Db	2887	TAGTGCATGCTTAACTGTCTCTCTCTCAAGACTCTGCTCTTATCTGTTTCTATTTTCTCTCC	2946
QY	2520	TTTTCCACCGAAGCTAATATCTCAGAAAGAGGAGCACTGGGCTTGAAGGCTCTGGGCT	2579
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QY	2580	AAGAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGTCTTACCCCTTGT	2639
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QY	2640	GATGAGAGAGCTCCCAAGGGGTTTGCTTTTTCATGTTACAGGCTTAACTCAGATCAACC	2699
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QY	2700	AGGGGCAAGAAAGAAAGTAACTTAACTTAATGCTGCTTAAATTTGTAATTTTGAAT	2759
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510	<800	560	<800	3756
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2597	2624	448	<800	2871
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4931	4857	6594	6656	8963
3907	3818	4503	4468	1945
8001	7718	5154	5136	1325
3804	3818	4730	4713	11341
2355	2376	13628	13324	975
862	868	166	<800	2501
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3900	3818	1613	1641	1756
1905	1854	1479	1503	883
7872	7718	1540	1503	1945
1174	1155	520	<800	1631
7015	7139	219	<800	3756
2852	2868	1571	1503	6551

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DB	84809	GGATCCCTACCTTCCCTCCATCAGAGCTAGGAGGAGCATGAGAGCGCTCTGTGTAATGAGGGA	84868
QY	61	CCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACAGATGGATGGCCAGTCCGTT	120
DB	84869	CCCCAAGAAATGTCTCCCTGTGGGCACTTCTTACAGATGGATGGCCAGTCCGTT	84928
QY	121	AAGTTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGACTTGTGAGATTCTCGGTTT	180
DB	84929	AAGTTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGACTTGTGAGATTCTCGGTTT	84988
QY	181	GTTCATGGATGGGAGGAGTCAAGAGCAGACGCTTGCTCAAGTCCATGATGCA	240
DB	84989	GTTCATGGATGGGAGGAGTCAAGAGCAGACGCTTGCTCAAGTCCATGATGCA	85048
QY	241	GGAAAAAGTGCATAGCTGGGCGCAGGCGCCCTGTGTGAGGCGTAGTGTAAACAGA	300
DB	85049	GGAAAAAGTGCATAGCTGGGCGCAGGCGCCCTGTGTGAGGCGTAGTGTAAACAGA	85108
QY	301	GAGGGCTCTCCATTCCAGCCCAAGGAAGCTAAGAAATGAATCTCATAGATATATTAGC	360
DB	85109	GAGGGCTCTCCATTCCAGCCCAAGGAAGCTAAGAAATGAATCTCATAGATATATTAGC	85168
QY	361	TCAAAACCAACAGAGGTTCCAGAAAAAGGCTCAGGTTGAAACAGGTCAACCCCAAC	420
DB	85169	TCAAAACCAACAGAGGTTCCAGAAAAAGGCTCAGGTTGAAACAGGTCAACCCCAAC	85228
QY	421	TCAGCAGACCAAGTCAATAAATCAAGAACCAAGAGCAGAGCAACCCCTTCCCA	480
DB	85229	TCAGCAGACCAAGTCAATAAATCAAGAACCAAGAGCAGAGCAACCCCTTCCCA	85288
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Qy 541 AAGGAACATGTAAAGAAAGAACTGAAATTATTAAGCTGACAGCTAAAGAGATGATAA 600
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Qy 960 AAGGCAATTTTGAAGCTTAATCAACCTCTCACTAATTTGATCTAAGTATCACTT 1019
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Db 85883 TATTTATTTATTTATTTATTTTGAAGATGAGTCTGCTGTCGCCCAAGCTGAGTGA 85942
Qy 1140 GGGGGGTATCAAGTTCATGAGCTCAACCTTTAGGCTCAAGGATTTCTCCCACT 1199
Db 85943 GGGGGGTATCAAGTTCATGAGCTCAACCTTTAGGCTCAAGGATTTCTCCCACT 86002
Qy 1200 CAGCCCCCAAGTATGTTGGGACCAACAGTATGCGCAGCATGCTGGCTAATTTCTTAT 1259
Db 86003 CAGCCCCCAAGTATGTTGGGACCAACAGTATGCGCAGCATGCTGGCTAATTTCTTAT 86062
Qy 1260 TTTTGTAGAGATGAGATCTCATATATTTGTCCAGGCTGTGCTTGAATTTCTGGGCTCAG 1319
Db 86063 TTTTGTAGAGATGAGATCTCATATATTTGTCCAGGCTGTGCTTGAATTTCTGGGCTCAG 86122
Qy 1320 GTGAGCTTCCCACTGGGCTCTCCCAAGTATCTGGGATTAAGGCAATGAGGCTGCC 1379
Db 86123 GTGAGCTTCCCACTGGGCTCTCCCAAGTATCTGGGATTAAGGCAATGAGGCTGCC 86182
Qy 1380 TSCCATATGAGATTTTCTGTCTCTGATCCATGACAGTATGATCAAGGACTTTGGCTGC 1439
Db 86183 TSCCATATGAGATTTTCTGTCTCTGATCCATGACAGTATGATCAAGGACTTTGGCTGC 86242
Qy 1440 TGACTCTGAGAGACTGCAATGCTTTCTTGAAGCTGTAAGCTTCAAGCTTAAAGCTATAG 1499
Db 86243 TGACTCTGAGAGACTGCAATGCTTTCTTGAAGCTGTAAGCTTCAAGCTTAAAGCTATAG 86302
Qy 1500 GGAAGCCCTGAACCCCAACCAAAAGGTTCTATGTTTATCAATCTGATCAATGTTGATTT 1559
Db 86303 GGAAGCCCTGAACCCCAACCAAAAGGTTCTATGTTTATCAATCTGATCAATGTTGATTT 86362
Qy 1560 ATGAAATTAACATGATTTAAAGACTTAACTCAACCTCAAGTGAACAAAATTAAATTT 1619

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Db 86663 CTGATGGAGACACACAAACCAATTTGTTCTCAAGTCCATTTTCTCTCAAAAGCTGAG 86722
Qy 1920 AATGTCCATTAATCAATGGAGATGATCTGACAGACCCATGAAGAAAGATCAACAG 1979
Db 86723 AATGTCCATTAATCAATGGAGATGATGATCTGACAGACCCATGAAGAAAGATCAACAG 86782
Qy 1980 TTCCACCCCAAGGAGCCCTATTTTCTCTAATTTCAATTTGAATAGGCTCTAATGTCCTTC 2039
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DB 87623 TGTGATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 87682
OY 2880 CTCAAGTCCTGTAAGCAAAATTTTCAAAAGTAAATTTAAATTTAAATTTGTAAT 2939
DB 87683 CTCAAGTCCTGTAAGCAAAATTTTCAAAAGTAAATTTAAATTTAAATTTGTAAT 87742
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DB 88103 TTAAGAAATCTGTATCTTATCTTCAACCAACCAACCAACCAACCAACCAACCA 88162
OY 3360 CATTGCC-GGTGATGCTGTAATCTTCAACCAACCAACCAACCAACCAACCAACCA 3418
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RESULT 7
ACI04439 ACI04439 197279 bp DNA linear PRI 20-JUN-2002
LOCUS Homo sapiens chromosome 3 clone RP11-793B15, complete sequence.
DEFINITION ACI04439 AC024739
ACCESSION ACI04439.2 GI:21490240
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS
Hominidae; Homo.
1 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kidukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kidukawa, M., Raymond, C.
and Haugen, E.D.
Direct Submission
Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:17488621.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgctg@u.washington.edu
Drafting Center: WUGSC
----- Project Information
Center project name: chr-3
Center clone name: RP11-793B15 (bc0564)
----- Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing method: plasmid; 108752; 48% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs
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Overlapping Sequences:

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5': RP11-9188 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)
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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered

361 TACAACCAACACACAGGTTCCAGAAAAAGGCTCAGCGTTGGAAACAAGTCAACCCCCAC 420
Db 186966 TAGAACAACCAACACAGGTTCCAGAAAAAGGCTCAGCGTTGGAAACAAGTCAACCCCCAC 187025
Qy 421 TCAGCAGACACACAGTCTATTAATCAAGACCAACAGGAGACAGGAAACCCCTTCCCA 480
Db 187026 TCAGCAGACACACAGTCTATTAATCAAGACCAACAGGAGACAGGAAACCCCTTCCCA 187085
Qy 481 CTCGCCCCAGTCTCAAGTTGAGTGGCCCTTCCCTCAGATCTCGCCACCATCTTGA 540
Db 187086 CTCGCCCCAGTCTCAAGTTGAGTGGCCCTTCCCTCAGATCTCGCCACCATCTTGA 187145
Qy 541 AAGAACACTGAGAAAGAACTGAAATTTAAGCTGACAGCATTAAGAGATGATTA 600
Db 187146 AAGAACACTGAGAAAGAACTGAAATTTAAGCTGACAGCATTAAGAGATGATTA 187205
Qy 601 ACCTTAAATCATTTGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 187206 ACCTTAAATCATTTGTCATGATGATGATGATGATGATGATGATGATGATGAT 187265
Qy 661 TGTGTGAATCTTTTCTGCTATCCAGAGATGAGAGCTGGTAAACAGACCAACATA 720
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HSA312688 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL COMMENT

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HSA312688      220965 bp      DNA      linear      HTG 15-MAY-2002
Homo sapiens chromosome 3 clone RP6-32923 map 3p21.3, ***
SEQUENCING IN PROGRESS ***, 26 ordered pieces.
AJ312688
AJ312688.2 GI:13559235
HTG; HTGS_PHSB2.
Homo sapiens (human)
SOURCE
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Kies, H., Yang, Y., Kies, C., Andersson, K., Klein, G., Imreh, S. and
Dumanek, J. P.
The transcriptional map of the common eliminated region 1 (C3CB1)
in 3p21.3
Eur. J. Hum. Genet. 10 (1), 52-61 (2002)
11896456
2 (bases 1 to 220965)
Kies, H.
Direct Submission
Submitted (01-APR-2001) Kies H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
On Apr 5, 2001 this sequence version replaced gi:13548633.
The sequence is a consensus sequence of clone RP4-787c23 (1-140400
bp), clone RP6-32923 (31212-220965 bp), clone RP6-146e1 (partially,
1-6800 bp)
and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
contigs are
in order and the gaps between them are represented by 100 Ns.
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117756-118727 bp
Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig
12:
127956-129383 bp Contig 13: 129484-131747 bp Contig 14:
131848-132316 bp
Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig
17:
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:
189577-191375 bp
Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
22:
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
213632-218109 bp
Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1
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11732 11831: gap of 100 bp
11832 26218: contig of 14387 bp in length
26219 26318: gap of 100 bp
26319 28347: contig of 2029 bp in length
28348 28447: gap of 100 bp
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42161 42360: gap of 200 bp
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VERSION AF224497.1 GI:13924486
SEGMENT 2 of 2
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REFERENCE 1 (bases 1 to 7010)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 7010)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland

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RESULT 11
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DEFINITION Sequence 310 from Patent WO200928.
ACCESSION AX345239
VERSION AX345239.1 GI:18493125
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SOURCE
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other sequences; artificial sequences.
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JOURNAL Patent: WO 0200928-A 310 03-JAN-2002;
Epigenomics AG (DE)
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Db	3725	TTTATAGTTCGATTAATTAATTTTATTAAGAAGTAAATAATATTTTTCGTATGTGTTTA	3784
Qy	2341	GTTATTAGCAATTCCTCGATTTTACCCTGAGAAAGCCATCGCGCTGTATTATCACATC	2400
Db	3785	GTTATTAGATTTTATTTTATTTGATTTATTTGAGAAAGTTTATCGGTTGTATATTTATTT	3844
Qy	2401	TTCAACCTGTGTCCTTCTCCTAGAAAGAGAAAGTCAGTTGATGACCTCTGAGAACT	2460
Db	3845	TTTATTTTGTGTTTTTTTTTTTGAAGAGAAAGATTAGTTGATGTTTTTGAAGAAAT	3904
Qy	2461	AGTCATGCGTTAACTGTCTTCCATGACCTCGCTTATCTGTTTCTATTTTCTCT	2520
Db	3905	AGTGTATGTTTAAATTTGTTTTTATTAAGATTTTGTATTATTTGTTTTTATTTTTTTTT	3964
Qy	2521	TTTCCACCGAAGCTCTATATCTCAAGAAAGACGACCTGCGCTTAAGGCTCTCGGCTTA	2580
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Qy	2581	AGAAATATCAAGTCCAGTGAGAAATCCCATTTGACTGACCCCTCGCTTACCCCTTTG	2640
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Qy	2701	GGGCGAAGAAAGAAAGTAACTTAATCTATGCTGTATTAATTGTATTTGTATTA	2760
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Qy	2761	GTTATTACTGTGATGTGCATGCTGTAACAGCAAAAGTGAATTTTTTTCACAGCTGT	2820
Db	4205	GTTATTAATTGTGATGTGATATGTGTAAATAGTAAATAGTATTTTTTTTATAGTGT	4264
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Qy	2881	TCAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATACATACATTTGATCTAGT	2940
Db	4325	TTAAGTTCGTGTAAATTTTTTAAAGTTAAATTTAAATTTATTTATTTTGAATTTAGT	4384
Qy	2941	GACAGGAATAATGACATGATATGACATTAAGATCTAGCCCAATTTTATTTTACTGTG	3000
Db	4385	GATAGAGAAATAGATATGATAGATTTAAAGATTATGTTAAATTTTATTTATTTATTTG	4444
Qy	3001	TTAGAGATTTTGAACAATTTCTAATTTCTTCAAGGTTCAATTTCCCATTAATCTATA	3060
Db	4445	TTAGAGATTTTGAATTAATTTATTAATTTTAAAGTTTAAATTTTATTTATTTATTA	4504
Qy	3061	ATGAATGTCATCATTAATGGGCGCTGAGAGACATTAATTTCTGTATTTGTAAATATC	3120
Db	4505	ATGAATGCTTAAATTTTAAATGGGTTTGGAGAAAGTAAATTAATTTGTAAATGTATTAAT	4564
Qy	3121	ATTGTATTAATTAATACATTTTGTGCTTTAAATGATGAAGATTTTAAAGGTAAAG	3180
Db	4565	ATTGTATTAATTAATTAATTAATTTTGTTTTAAATGATGAAGATTTTAAAGGTAAAG	4624
Qy	3181	TAAACTGTAAACATTAATATGCAAAATGCGGTAAAGACAGTATGATTAATATGATTA	3240
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Accession	Sequence	Position
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QY	3420 CACCTCGATATGCTTTTGAATAATCATGTTAAAGATTCCTGAGCGTATACATGTG	3479
D6	4865 TATTTTGAATATGTTTTTGAATTTATGTTAAAGAAATTTTAAAGTGTATATATATG	4924
QY	3480 GCATCTTGTGTAGTACATGATTAATCAATCGGTGTGTTTTTACGAAGATGATTAAGT	3539
D6	4925 GATTTTTTGTGAATATATGATTAATTAATTAATGCTGTGTTTACGAAGATGATTAAGTT	4984
QY	3540 TCATTTGGGATGTGATTTTTTCTCTCTCTATCAAGGAGAGAGTAA	3586
D6	4985 TTATTTGGGATGTGATTTTTTTTTTTTTTATTTATGAGGAGAGAGTAA 5031	

RESULT	13
LOCUS	AF262300
DEFINITION	Homo sapiens clone 2 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION	AF262300
VERSION	AF262300.1
KEYWORDS	GI:19171642
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE AUTHORS	TITLE	JOURNAL PUBMED
1 (bases 1 to 1310) Vijh.S., Dayhoff,D.E., Wang,C.B., Imam,Z., Ehrenberg,P.K. and Michael,N.L.	Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rate TATA-less Promoter Structure Conserved between Drosophila and Humans	Genomics 80 (1), 86-95 (2002) 12079287
2 (bases 1 to 1310) Vijh.S., Dayhoff,D.E., Wang,C.B., Ehrenberg,P.K. and Michael,N.L.	Direct Submission	Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
REFERENCE AUTHORS TITILE JOURNAL	Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA	

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FEATURES
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